GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 19:57:17 ; Search time 4103.41 Seconds
(without alignments)
12684.514 Million cell updates/sec

Title: US-10-077-698-2
Perfect score: 1743
Sequence: 1 tccggactagttctagaccg.....aaaaaaaaaaaaaagggcgg 1743

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	33.4	936	14	CD517915	CD517915 AGENCOURT
2	508	29.1	611	12	BM739118	BM739118 K-EST0008
3	393	22.5	1201	13	BX444304	BX444304 BX444304
4	343	19.7	448	12	BM757151	BM757151 K-EST0035
c 5	172	9.9	442	9	AI469384	AI469384 tm08a12.x
6	67	3.8	291	10	BF924587	BF924587 IL5-NT022
c 7	65	3.7	451	14	R44593	R44593 yg23e12.s1
c 8	60	3.4	602	10	AW973354	AW973354 EST385497
c 9	59	3.4	229	9	AA558426	AA558426 nk38c09.s
c 10	59	3.4	446	13	BX506188	BX506188 DKFZp686O
11	57	3.3	637	10	BE061278	BE061278 IL0-BT016
c 12	57	3.3	779	14	CD644362	CD644362 AGENCOURT
13	56	3.2	637	14	CB448183	CB448183 702244 MA
14	56	3.2	1287	11	BC017579	BC017579 Homo sapi
15	55	3.2	208	13	BU660876	BU660876 cl65d10.z
c 16	55	3.2	352	9	AA421536	AA421536 zu07d09.r
c 17	55	3.2	417	9	AI584031	AI584031 ts12g07.x
c 18	55	3.2	437	28	AQ192617	AQ192617 HS_2247_B
19	55	3.2	470	12	BM257564	BM257564 521229 MA
20	53	3.0	276	10	BE005691	BE005691 RC2-BN012
c 21	53	3.0	340	14	F00574	F00574 HSB13C062 S
22	53	3.0	341	14	T70034	T70034 yc17a08.s1
c 23	53	3.0	604	10	AW511652	AW511652 xu80d03.x
24	52	3.0	313	9	AA557984	AA557984 nl26h04.s
25	52	3.0	381	12	BG547663	BG547663 602575508
26	52	3.0	657	29	AG103735	AG103735 Pan trogl
27	52	3.0	696	14	CB270068	CB270068 1008975 H
c 28	52	3.0	863	10	BF671675	BF671675 602151534
c 29	51	2.9	410	9	AI559474	AI559474 tq44d03.x
30	51	2.9	553	9	AL134346	AL134346 DKFZp547P
31	51	2.9	877	9	AU121388	AU121388 AU121388
32	51	2.9	1177	13	BX381249	BX381249 BX381249
c 33	50	2.9	261	14	F08214	F08214 HSCZOC071 n
c 34	50	2.9	299	28	B84381	B84381 RPCI11-24D2
c 35	50	2.9	303	9	AA807579	AA807579 nw26d04.s
c 36	50	2.9	306	9	AA713765	AA713765 nv82e07.s
c 37	50	2.9	308	12	BG323887	BG323887 602422916
c 38	50	2.9	309	14	F08655	F08655 HSC1HC091 n
39	50	2.9	322	28	AQ195340	AQ195340 RPCI11-61
c 40	50	2.9	331	14	T40700	T40700 ya09b06.s1
41	50	2.9	332	10	BF129140	BF129140 601811407
42	50	2.9	340	13	BU957861	BU957861 AGENCOURT
43	50	2.9	348	9	AA632556	AA632556 np81g02.s
44	50	2.9	348	13	BX485913	BX485913 DKFZp686E
c 45	50	2.9	361	28	AZ694901	AZ694901 UP_523-17

ALIGNMENTS

RESULT 1
CD517915
LOCUS CD517915 936 bp mRNA linear EST 06-JUN-2003
DEFINITION AGENCOURT_14364614 NIH_MGC_181 Homo sapiens cDNA clone IMAGE:30397270 5', mRNA sequence.
ACCESSION CD517915
VERSION CD517915.1 GI:31449633
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 936)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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            http://image.llnl.gov
            Plate: NDAM480  row: e  column: 23
            High quality sequence stop: 684.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:30397270"
                     /tissue_type="White Matter"
                     /dev_stage="Unknown"
                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_181"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV
                     (destroyed); Library is oligo-dT primed and directionally
                     cloned (EcoRV site is destroyed upon cloning). Average
                     insert size 1.42 kb. Library was constructed by
                     (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             33.4%;  Score 582;  DB 14;  Length 936;
  Best Local Similarity   99.7%;  Pred. No. 9.1e-106;
  Matches  682;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         74 GACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGAC 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGAC 60

Qy        134 GTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATC 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATC 120

Qy        194 TTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGC 253
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        121 TTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGTGCCGACGACGC 180

Qy        254 CGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGC 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGC 240

Qy        314 GCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCC 300

Qy        374 TGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCC 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCC 360

Qy        434 GCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCT 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCT 420

Qy        494 GGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCT 553
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Db        421 GGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCT 480

Qy        554 CTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAA 613
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 CTGCCTCTCTGCGTCTTCTTCCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAA 540

Qy        614 ATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCT 673
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Db        541 ATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCT 600

Qy        674 TTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATT 733
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Db        601 TTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATT 660

Qy        734 TTACAGATCACAAAGGCATCAAGG 757
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Db        661 TTACAGATCACAAAGGCATCAAGG 684
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RESULT 2
BM739118
LOCUS       BM739118                611 bp    mRNA    linear   EST 01-MAR-2002
DEFINITION  K-EST0008503 S3SNU16 Homo sapiens cDNA clone S3SNU16-3-B11 5', mRNA
            sequence.
ACCESSION   BM739118
VERSION     BM739118.1  GI:19060447
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 611)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 3  row: B  column: 11
            High quality sequence stop: 611.
FEATURES             Location/Qualifiers
     source          1. .611
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S3SNU16-3-B11"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-16"
                     /lab_host="Top10F'"
                     /clone_lib="S3SNU16"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match             29.1%;  Score 508;  DB 12;  Length 611;
  Best Local Similarity   99.8%;  Pred. No. 4.6e-91;
  Matches  558;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 87

Qy         75 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 147

Qy        135 TCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCT 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 TCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCT 207
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Qy        195 TTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCC 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        208 TTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGTGCCGACGACGCC 267

Qy        255 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 314
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Db        268 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 327

Qy        315 CTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCT 374
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Db        328 CTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCT 387

Qy        375 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCG 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCG 447

Qy        435 CGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTG 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 CGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTG 507

Qy        495 GGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTC 554
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Db        508 GGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTC 567

Qy        555 TGCCTCTCTGCGTCTTCTT 573
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Db        568 TGCCTCTCTGCGTCTTCTT 586
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RESULT 3
BX444304
LOCUS       BX444304               1201 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX444304 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
            CS0DN001YC21 5-PRIME, mRNA sequence.
ACCESSION   BX444304
VERSION     BX444304.1  GI:30776199
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 5904.f,
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DN001AB11QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN001YC21"
                     /tissue_type="ADULT BRAIN"
                     /dev_stage="adult"
                     /clone_lib="Homo sapiens ADULT BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN
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  Query Match            22.5%;  Score 393;  DB 13;  Length 1201;
  Best Local Similarity  99.2%;  Pred. No. 9.8e-69;
  Matches  643;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
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Qy         92 CTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGG 151
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Db        152 CTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGG 211

Qy        152 CTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTG 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTG 271

Qy        212 GGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGC 271
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        272 GGCAACGTGTGCGCCCTGGTGCTGGTGGCGTGCCGACGACGCCGCGGCGCGACTGCCTGC 331

Qy        272 CTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTG 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 CTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTG 391

Qy        332 GCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTAC 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTAC 451

Qy        392 GTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGC 451
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        452 GTGATGACCCTGAGCGGCAGCKNCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGC 511

Qy        452 ATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCA 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 ATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCA 571

Qy        512 GTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTC 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTC 631

Qy        572 TTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTG 631
              || |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        632 TTCCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGAACAGGAAATTTCGATTTGCACACTG 691

Qy        632 ATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTC 691
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Db        692 ATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTC 751

Qy        692 TTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 739
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Db        752 TTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 799
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RESULT 4
BM757151
LOCUS       BM757151               448 bp    mRNA    linear   EST 04-MAR-2002
DEFINITION  K-EST0035924 S3SNU16 Homo sapiens cDNA clone S3SNU16-31-B04 5',
            mRNA sequence.
ACCESSION   BM757151
VERSION     BM757151.1  GI:19086766
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 31  row: B  column: 04
            High quality sequence stop: 448.
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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-16"
                     /lab_host="Top10F'"
                     /clone_lib="S3SNU16"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match            19.7%;  Score 343;  DB 12;  Length 448;
  Best Local Similarity  99.7%;  Pred. No. 1.6e-58;
  Matches  393;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 87

Qy         75 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 147

Qy        135 TCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCT 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 TCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCT 207

Qy        195 TTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCC 254
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        208 TTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGTGCCGACGACGCC 267

Qy        255 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 327

Qy        315 CTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCT 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 CTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCT 387

Qy        375 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGG 408
              |||||||||||||||||||||||||||||||||
Db        388 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGG 421


RESULT 5
AI469384/c
LOCUS       AI469384                442 bp    mRNA    linear   EST 14-APR-1999
DEFINITION  tm08a12.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2155966 3'
            similar to contains Alu repetitive element;contains element THR
            repetitive element ;, mRNA sequence.
ACCESSION   AI469384
VERSION     AI469384.1  GI:4331474
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 777   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 401.
FEATURES             Location/Qualifiers
     source          1. .442
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2155966"
                     /tissue_type="moderately-differentiated adenocarcinoma"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Co14"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.7 kb. Life Technologies catalog #:
                     11531-019"
ORIGIN

  Query Match             9.9%;  Score 172;  DB 9;  Length 442;
  Best Local Similarity  100.0%;  Pred. No. 6.3e-25;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1286 AAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCAGTGGTTCATGC 1345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCAGTGGTTCATGC 383

Qy       1346 CTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGA 1405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 CTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGA 323

Qy       1406 GACCAACCTGACCAACATGGTGAGACCCCCGTCTCTACTAAAAATAAAAAAA 1457
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 GACCAACCTGACCAACATGGTGAGACCCCCGTCTCTACTAAAAATAAAAAAA 271


RESULT 6
BF924587
LOCUS       BF924587                291 bp    mRNA    linear   EST 19-JAN-2001
DEFINITION  IL5-NT0228-271100-271-h06 NT0228 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF924587
VERSION     BF924587.1  GI:12320473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 291)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
```

```
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&t2=IL5-NT0228-
            271100-271-h06&t3=2000-11-27&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 290.
FEATURES             Location/Qualifiers
     source          1. .291
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NT0228"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             3.8%;  Score 67;  DB 10;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 0.00039;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1344 GCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTC 1403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTC 196

Qy       1404 GAGACCA 1410
             |||||||
Db        197 GAGACCA 203


RESULT 7
R44593/c
LOCUS       R44593                   451 bp    mRNA    linear   EST 22-MAY-1995
DEFINITION  yg23e12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone
            IMAGE:33011 3' similar to contains Alu repetitive element;, mRNA
            sequence.
ACCESSION   R44593
VERSION     R44593.1  GI:823981
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 9, 1995 this sequence version replaced gi:803317.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1494
            High quality sequence stops: 370 Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1494   Std Error: 0.00
            Seq primer: Promega -21m13
            High quality sequence stop: 370.
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:405358"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:33011"
                     /sex="female"
                     /dev_stage="73 days post natal"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares infant brain 1NIB"
                     /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                     I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                     I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTT 3']
                     double-stranded cDNA was ligated to Hind III adaptors
                     (Pharmacia), digested with Not I and directionally cloned
                     into the Not I and Hind III sites of the Lafmid BA vector.
                     Library went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             3.7%;  Score 65;  DB 14;  Length 451;
  Best Local Similarity   100.0%;  Pred. No. 0.00064;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1344 GCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTC 1403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 GCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTC 216

Qy       1404 GAGAC 1408
             |||||
Db        215 GAGAC 211


RESULT 8
AW973354/c
LOCUS       AW973354                 602 bp    mRNA    linear   EST 02-JUN-2000
DEFINITION  EST385497 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW973354
VERSION     AW973354.1  GI:8164576
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
            Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 318
            Seq primer: Forward.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
```

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                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGM"
                     /note="Vector: pBluescriptSKm"
ORIGIN

  Query Match             3.4%;  Score 60;  DB 10;  Length 602;
  Best Local Similarity   100.0%;  Pred. No. 0.0048;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1351 ATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 1410
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 ATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 194


RESULT 9
AA558426/c
LOCUS       AA558426                 229 bp    mRNA    linear   EST 08-SEP-1997
DEFINITION  nk38c09.s1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1015792 3'
            similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION   AA558426
VERSION     AA558426.1  GI:2328903
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 229)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
            Ph.D.
            cDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1192   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 218.
FEATURES             Location/Qualifiers
     source          1. .229
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1015792"
                     /tissue_type="germ cell tumor"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="NCI_CGAP_GC2"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Cloned unidirectionally.  Primer: Oligo dT. Bulk
                     germ cell tumor. 5' adaptor sequence: 5' GAATTCGGCACGAG 3'
                     3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'
                     Average insert size:  1.2 kb."
ORIGIN

  Query Match             3.4%;  Score 59;  DB 9;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1352 TCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 1410
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 TCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 171


RESULT 10
BX506188/c
LOCUS       BX506188                 446 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686O24221_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686O24221 5', mRNA sequence.
ACCESSION   BX506188
VERSION     BX506188.1  GI:32037167
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 446)
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,
            Wellenreuther,R., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686O24221) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .446
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686O24221"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

  Query Match             3.4%;  Score 59;  DB 13;  Length 446;
  Best Local Similarity   100.0%;  Pred. No. 0.0098;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1345 CCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTC 1403
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 CCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTC 236


RESULT 11
BE061278
LOCUS       BE061278                 637 bp    mRNA    linear   EST 09-JUN-2000
DEFINITION  IL0-BT0168-031199-135-a05 BT0168 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE061278
VERSION     BE061278.1  GI:8405928
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
```

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   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=IL0-BT0168-031
            199-135-a05&t3=1999-11-03&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 637.
FEATURES             Location/Qualifiers
     source          1. .637
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="BT0168"
                     /note="Organ: breast; Vector: pUC18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

  Query Match             3.3%;  Score 57;  DB 10;  Length 637;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1340 TCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCA 1396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCA 432


RESULT 12
CD644362/c
LOCUS       CD644362                779 bp    mRNA    linear   EST 17-JUN-2003
DEFINITION  AGENCOURT_14553420 NIA Human H1 Embryonic Stem Cell cDNA Library
            (Long) Homo sapiens cDNA clone IMAGE:30424873 5', mRNA sequence.
ACCESSION   CD644362
VERSION     CD644362.1  GI:31816168
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 779)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
             cDNA Library Preparation: Yulan Piao and Minoru Ko
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC c           lone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM508  row: d  column: 02
            High quality sequence stop: 650.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:30424873"
                     /tissue_type="Embryonic Stem cells"
                     /cell_line="WA01"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library
                     (Long)"
                     /note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI;
                     This is a long-transcript enriched cDNA library (Genome
                     Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01
                     cell line .  Undifferentiated human ES cell line WA01/H1
                     was obtained from WiCell Research Institute, Inc.,
                     Madison, Wi, cultured according to their instructions, on
                     MEF feeders. They formed round colonies with defined edges
                     and were positive for alkaline phosphatase, SSEA-4, OCT3,
                     OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45.  They are
                     negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1,
                     TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days
                     after plating), the ES cells from 4 X 6cm dishes were
                     treated with 1 mg/ml collagenase, type IV
                     (Invitrogen/GIBCO) for 5-10 min and gently scraped off
                     with 5 ml pipette.  RNA was purified with TRIzol Reagent
                     from Invitrogen. Protocol ref:  Genome Res. 11: 1553-1558
                     (2001). [PMID:11544199]) Double-stranded cDNAs were
                     synthesized with an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                     3.4g of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform
                     extraction, and separated from free linkers by
                     Centricon-100 column.  Then, the cDNAs were amplified by
                     long-range high fidelity PCR using Ex Taq polymerase
                     (Takara) with a primer Sal4-S for 25 cycles.  The products
                     were purified by phenol/chloroform extraction and
                     Centricon-100 column. The cDNAs were digested with SalI
                     and NotI enzymes and cloned into SalI/NotI site of
                     pCMV-SPORT6 plasmid vector. The average insert size is
                     about 3.6kb."
ORIGIN

  Query Match             3.3%;  Score 57;  DB 14;  Length 779;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1340 TCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCA 1396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCA 300


RESULT 13
CB448183
LOCUS       CB448183                637 bp    mRNA    linear   EST 26-MAR-2003
DEFINITION  702244 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB448183
VERSION     CB448183.1  GI:29254565
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
```

```
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8057  row: L  column: 17
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES              Location/Qualifiers
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                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /clone_lib="MARC 6BOV"
                      /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                      Library made with RNA pooled from multiple tissues
                      including liver, lung, hypothalamus, pituitary, and
                      placenta/endometrium."
ORIGIN

  Query Match             3.2%;  Score 56;  DB 14;  Length 637;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        857 TCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCA 912
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Db        260 TCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCA 315


RESULT 14
BC017579
LOCUS       BC017579               1287 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:4107433, mRNA.
ACCESSION   BC017579
VERSION     BC017579.1  GI:17068402
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 32 Row: c Column: 11
            This clone has the following problem: retained intron.
FEATURES              Location/Qualifiers
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                      /clone="IMAGE:4107433"
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                      /clone_lib="NIH_MGC_55"
                      /lab_host="DH10B"
                      /note="Vector: pDNR-LIB"
ORIGIN

  Query Match             3.2%;  Score 56;  DB 11;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1516 CAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 1571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1164 CAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 1219


RESULT 15
BU660876
LOCUS       BU660876               208 bp    mRNA    linear   EST 30-SEP-2002
DEFINITION  cl65d10.z1 Hembase; Erythroid Precursor Cells (LCB:cl library) Homo
            sapiens cDNA clone cl65d10 5', mRNA sequence.
ACCESSION   BU660876
VERSION     BU660876.1  GI:23373058
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 208)
  AUTHORS   Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
  TITLE     Gene Expression in Human Erythroid Precursor Cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Jeffery L. Miller
            Laboratory of Chemical Biology
            National Institute of Diabetes and Digestive and Kidney Diseases
            Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
            20892, USA
            Tel: 301 402 2373
            Fax: 301 435 5148
            Email: jm7f@nih.gov
            The 'cl' library was constructed by Alexander Gubin, Ph.D. in the
            Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
            analyses by National Institutes of Health Intramural Sequencing
            Center (NISC). More information available at:
            http://hembase.niddk.nih.gov
            Plate: 65  row: d  column: 10
            Seq primer: 5' lambda-TriplEx2 Sequencing Primer.
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                      /sex="unknown"
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                      /cell_type="Erythroid Precursor Cells"
                      /cell_line="Primary Culture of Peripheral Blood
                      Mononuclear Cells"
                      /dev_stage="Precursor erythroblasts; GPA++"
                      /lab_host="DH5alpha"
                      /clone_lib="Hembase; Erythroid Precursor Cells (LCB:cl
                      library)"
                      /note="Organ: blood; Vector: pTriplEx2; Site_1: SfiI;
                      Site_2: SfiI; A complementary DNA (cDNA) library from
                      human erythroid precursor cells was constructed using
                      SMART PCR (polymerase chain reaction) cDNA Library
                      Construction Kit (Clontech, Palo Alto, CA) according to
                      the manufacturer's directions, but with slight
                      modifications. Briefly, reverse transcription was
                      performed in the presence of 1 umol/L peptide nucleic acid
                      (PNA) oligos
                      (N-terminal)-biotin-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and
                      (N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A-(C-terminal)
                      . Synthesized cDNA was digested with SfiI and
                      size-selected on a 1% agarose gel (>800bp). Large-scale
                      sequencing of the library was performed by the NIH
                      Intramural Sequencing Center (NISC;
                      Http://www.nisc.nih.gov/)."
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ORIGIN

Query Match 3.2%; Score 55; DB 13; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        128 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGCACTCCA 182
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Search completed: October 1, 2004, 03:51:44
Job time : 4109.41 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 21:45:48 ; Search time 123.742 Seconds
(without alignments)
6996.194 Million cell updates/sec

Title: US-10-077-698-5
Perfect score: 1560
Sequence: 1 ttgccaagctcagcgtaagc.....aaaaaaaaaaaaaaaaaaa 1560

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1560	100.0	1560	4	US-09-261-599B-5	Sequence 5, Appli
	2	1560	100.0	1560	4	US-09-456-455A-5	Sequence 5, Appli
	3	181	11.6	181	4	US-09-456-455A-14	Sequence 14, Appl
	4	138	8.8	138	4	US-09-456-455A-15	Sequence 15, Appl
	5	44	2.8	1743	4	US-09-261-599B-2	Sequence 2, Appli
	6	44	2.8	1743	4	US-09-456-455A-2	Sequence 2, Appli
	7	38	2.4	241	3	US-09-328-111-472	Sequence 472, App
	8	26	1.7	753	3	US-09-232-191-14	Sequence 14, Appl
	9	26	1.7	753	3	US-09-232-200-14	Sequence 14, Appl
	10	26	1.7	753	4	US-09-232-197-14	Sequence 14, Appl
	11	26	1.7	753	4	US-09-232-201-14	Sequence 14, Appl
	12	26	1.7	753	4	US-09-232-195-14	Sequence 14, Appl
c	13	26	1.7	1560	4	US-09-261-599B-5	Sequence 5, Appli
c	14	26	1.7	1560	4	US-09-456-455A-5	Sequence 5, Appli
	15	26	1.7	16442	3	US-08-781-891-208	Sequence 208, App
	16	26	1.7	16442	4	US-09-618-166-208	Sequence 208, App
c	17	25	1.6	624	3	US-09-385-982-414	Sequence 414, App
	18	25	1.6	694	4	US-09-148-545-23	Sequence 23, Appl
	19	25	1.6	960	3	US-09-248-335-57	Sequence 57, Appl
	20	25	1.6	994	4	US-09-366-887A-5	Sequence 5, Appli
	21	25	1.6	1174	4	US-10-164-595-49	Sequence 49, Appl
	22	25	1.6	1243	4	US-09-731-924A-1	Sequence 1, Appli
	23	25	1.6	1244	4	US-08-916-442-1	Sequence 1, Appli
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	26	25	1.6	1545	4	US-09-559-023-1	Sequence 1, Appli
	27	25	1.6	1594	4	US-09-016-434-1059	Sequence 1059, Ap
	28	25	1.6	1799	3	US-09-329-633A-1	Sequence 1, Appli
	29	25	1.6	1799	4	US-09-079-029-2	Sequence 2, Appli
	30	25	1.6	2140	3	US-09-058-389A-6	Sequence 6, Appli
	31	25	1.6	2140	4	US-09-611-781-6	Sequence 6, Appli
	32	25	1.6	2880	3	US-09-115-954-3	Sequence 3, Appli
	33	25	1.6	2920	4	US-10-158-847-137	Sequence 137, App
	34	25	1.6	3842	3	US-09-115-954-7	Sequence 7, Appli
	35	25	1.6	3912	3	US-09-115-954-1	Sequence 1, Appli
c	36	25	1.6	11050	4	US-10-204-708-86	Sequence 86, Appl
c	37	25	1.6	49136	3	US-09-422-869-1	Sequence 1, Appli
c	38	25	1.6	81001	4	US-09-750-580-1	Sequence 1, Appli
	39	25	1.6	148567	4	US-09-801-876B-3	Sequence 3, Appli
	40	25	1.6	148567	4	US-10-254-869-3	Sequence 3, Appli
c	41	25	1.6	152331	3	US-09-128-155-16	Sequence 16, Appl
	42	25	1.6	176373	3	US-09-128-155-17	Sequence 17, Appl
	43	25	1.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
	44	25	1.6	246240	2	US-08-724-394A-21	Sequence 21, Appl
	45	25	1.6	246240	2	US-08-724-394A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-261-599B-5
; Sequence 5, Application US/09261599B
; Patent No. 6395877
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 14273 Receptor, A No. 6395877el G-Protein Coupled Receptor
; FILE REFERENCE: 5800-4B, 035800/177086
; CURRENT APPLICATION NUMBER: US/09/261,599B
; CURRENT FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/107,761
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Murine ortholog
US-09-261-599B-5

Query Match 100.0%; Score 1560; DB 4; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
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Db         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120

Qy        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
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Db        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180

Qy        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
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Db        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240

Qy        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
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Db        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300

Qy        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
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Db        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
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Qy       361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
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Qy       421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
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Db       421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480

Qy       481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
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Qy       541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600
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Qy       601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660
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Qy       661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720

Qy       721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780

Qy       781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840
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Db       781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840

Qy       841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
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Db       841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900

Qy       901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
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Qy       961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020
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Qy      1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080

Qy      1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140

Qy      1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
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Db      1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200

Qy      1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260

Qy      1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320

Qy      1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380

Qy      1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440

Qy      1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500

Qy      1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
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RESULT 2
US-09-456-455A-5
; Sequence 5, Application US/09456455A
; Patent No. 6448005
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: 14273 Receptor, A No. 6448005el G-Protein Coupled Receptor
; FILE REFERENCE: MNI-204CP3
; CURRENT APPLICATION NUMBER: US/09/456,455A
; CURRENT FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 09/107,761
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Murine ortholog
US-09-456-455A-5

Query Match 100.0%; Score 1560; DB 4; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60

Qy        61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120

Qy       121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180

Qy       181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240

Qy       241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300

Qy       301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360

Qy       361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420

Qy       421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480

Qy       481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540

Qy       541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600

Qy        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660

Qy        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720

Qy        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780

Qy        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840

Qy        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900

Qy        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960

Qy        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200

Qy       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260

Qy       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320

Qy       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380

Qy       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440

Qy       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500

Qy       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
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RESULT 3
US-09-456-455A-14
; Sequence 14, Application US/09456455A
; Patent No. 6448005
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: 14273 Receptor, A No. 6448005el G-Protein Coupled Receptor
;  FILE REFERENCE: MNI-204CP3
;  CURRENT APPLICATION NUMBER: US/09/456,455A
;  CURRENT FILING DATE:  1999-12-08
;  PRIOR APPLICATION NUMBER: 09/107,761
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: 09/223,538
;  PRIOR FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 181
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-456-455A-14

  Query Match             11.6%;  Score 181;  DB 4;  Length 181;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-73;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 60

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 120

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 180

Qy       1201 G 1201
              |
Db        181 G 181


RESULT 4
US-09-456-455A-15
; Sequence 15, Application US/09456455A
; Patent No. 6448005
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: 14273 Receptor, A No. 6448005el G-Protein Coupled Receptor
;  FILE REFERENCE: MNI-204CP3
;  CURRENT APPLICATION NUMBER: US/09/456,455A
;  CURRENT FILING DATE:  1999-12-08
;  PRIOR APPLICATION NUMBER: 09/107,761
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: 09/223,538
;  PRIOR FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 138
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-456-455A-15

  Query Match              8.8%;  Score 138;  DB 4;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-53;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        909 AAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAA 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAA 60

Qy        969 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 120
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Qy       1029 CCCATCATCATCACCATC 1046
              ||||||||||||||||||
Db        121 CCCATCATCATCACCATC 138


RESULT 5
US-09-261-599B-2
; Sequence 2, Application US/09261599B
; Patent No. 6395877
; GENERAL INFORMATION:
;  APPLICANT:  Glucksmann, Maria A.
;  TITLE OF INVENTION:  14273 Receptor, A No. 6395877el G-Protein Coupled Receptor
;  FILE REFERENCE:  5800-4B, 035800/177086
;  CURRENT APPLICATION NUMBER: US/09/261,599B
;  CURRENT FILING DATE:  1999-02-26
;  PRIOR APPLICATION NUMBER:  09/107,761
;  PRIOR FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  09/223,538
;  PRIOR FILING DATE:  1998-12-30
;  NUMBER OF SEQ ID NOS:  7
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1743
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-261-599B-2

  Query Match             2.8%;  Score 44;  DB 4;  Length 1743;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-10;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 744


RESULT 6
US-09-456-455A-2
; Sequence 2, Application US/09456455A
; Patent No. 6448005
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: 14273 Receptor, A No. 6448005el G-Protein Coupled Receptor
;  FILE REFERENCE: MNI-204CP3
;  CURRENT APPLICATION NUMBER: US/09/456,455A
;  CURRENT FILING DATE:  1999-12-08
;  PRIOR APPLICATION NUMBER: 09/107,761
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: 09/223,538
;  PRIOR FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1743
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-456-455A-2

  Query Match             2.8%;  Score 44;  DB 4;  Length 1743;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-10;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 744


RESULT 7
US-09-328-111-472
; Sequence 472, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 472
;   LENGTH: 241
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-328-111-472

  Query Match             2.4%;  Score 38;  DB 3;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-08;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATC 71
              |||||||||||||||||||||||||||||||||||||
Db        101 ATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATC 138


RESULT 8
US-09-232-191-14
; Sequence 14, Application US/09232191
; Patent No. 6284487
; GENERAL INFORMATION:
;  APPLICANT: Stahl, Andreas
;  APPLICANT: Hirsch, David J.
;  APPLICANT: Lodish, Harvey F.
;  TITLE OF INVENTION: Fatty Acid Transport Proteins
;  FILE REFERENCE: WHI97-21p3ME
;  CURRENT APPLICATION NUMBER: US/09/232,191
;  CURRENT FILING DATE: 1999-01-14
;  EARLIER APPLICATION NUMBER: 60/071,374
;  EARLIER FILING DATE: 1998-01-15
;  EARLIER APPLICATION NUMBER: 60/093,491
;  EARLIER FILING DATE: 1998-07-20
;  EARLIER APPLICATION NUMBER: 60/110,941
;  EARLIER FILING DATE: 1998-12-04
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 753
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-232-191-14

  Query Match             1.7%;  Score 26;  DB 3;  Length 753;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1535 CCTACAAAAAAAAAAAAAAAAAAAAA 1560
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Db        726 CCTACAAAAAAAAAAAAAAAAAAAAA 751


RESULT 9
US-09-232-200-14
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; Sequence 14, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
;  APPLICANT: Stahl, Andreas
;  APPLICANT: Hirsch, David J.
;  APPLICANT: Lodish, Harvey F.
;  APPLICANT: Gimeno, Ruth E.
;  APPLICANT: Tartaglia, Louis A.
;  TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
;  FILE REFERENCE: WHI97-21p3MB
;  CURRENT APPLICATION NUMBER: US/09/232,200A
;  CURRENT FILING DATE: 1999-01-14
;  EARLIER APPLICATION NUMBER: 60/071,374
;  EARLIER FILING DATE: 1998-01-15
;  EARLIER APPLICATION NUMBER: 60/093,491
;  EARLIER FILING DATE: 1998-07-20
;  EARLIER APPLICATION NUMBER: 60/110,941
;  EARLIER FILING DATE: 1998-12-04
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 753
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-232-200-14

  Query Match             1.7%;  Score 26;  DB 3;  Length 753;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1535 CCTACAAAAAAAAAAAAAAAAAAAAA 1560
             |||||||||||||||||||||||||||
Db        726 CCTACAAAAAAAAAAAAAAAAAAAAA 751


RESULT 10
US-09-232-197-14
; Sequence 14, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
;  APPLICANT: Stahl, Andreas
;  APPLICANT: Hirsch, David J.
;  APPLICANT: Lodish, Harvey F.
;  APPLICANT: Gimeno, Ruth E.
;  APPLICANT: Tartaglia, Louis A.
;  TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
;  FILE REFERENCE: WHI97-21p3MA
;  CURRENT APPLICATION NUMBER: US/09/232,197A
;  CURRENT FILING DATE: 1999-01-14
;  EARLIER APPLICATION NUMBER: 60/071,374
;  EARLIER FILING DATE: 1998-01-15
;  EARLIER APPLICATION NUMBER: 60/093,491
;  EARLIER FILING DATE: 1998-07-20
;  EARLIER APPLICATION NUMBER: 60/110,941
;  EARLIER FILING DATE: 1998-12-04
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 753
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-232-197-14

  Query Match             1.7%;  Score 26;  DB 4;  Length 753;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1535 CCTACAAAAAAAAAAAAAAAAAAAAA 1560
             |||||||||||||||||||||||||||
Db        726 CCTACAAAAAAAAAAAAAAAAAAAAA 751


RESULT 11
US-09-232-201-14
; Sequence 14, Application US/09232201A
; Patent No. 6348321
; GENERAL INFORMATION:
;  APPLICANT: Stahl, Andreas
;  APPLICANT: Hirsch, David J.
;  APPLICANT: Lodish, Harvey F.
;  APPLICANT: Gimeno, Ruth E.
;  APPLICANT: Tartaglia, Louis A.
;  TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
;  FILE REFERENCE: WHI97-21p3MC
;  CURRENT APPLICATION NUMBER: US/09/232,201A
;  CURRENT FILING DATE: 1999-01-14
;  EARLIER APPLICATION NUMBER: 60/071,374
;  EARLIER FILING DATE: 1998-01-15
;  EARLIER APPLICATION NUMBER: 60/093,491
;  EARLIER FILING DATE: 1998-07-20
;  EARLIER APPLICATION NUMBER: 60/110,941
;  EARLIER FILING DATE: 1998-12-04
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 753
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-232-201-14

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Db        726 CCTACAAAAAAAAAAAAAAAAAAAAA 751


RESULT 12
US-09-232-195-14
; Sequence 14, Application US/09232195A
; Patent No. 6657049
; GENERAL INFORMATION:
;  APPLICANT: Stahl, Andreas
;  APPLICANT: Hirsch, David J.
;  APPLICANT: Lodish, Harvey F.
;  APPLICANT: Gimeno, Ruth E.
;  APPLICANT: Tartaglia, Louis A.
;  TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
;  FILE REFERENCE: WHI97-21p3MD
;  CURRENT APPLICATION NUMBER: US/09/232,195A
;  CURRENT FILING DATE: 1999-01-04
;  EARLIER APPLICATION NUMBER: 60/071,374
;  EARLIER FILING DATE: 1998-01-15
;  EARLIER APPLICATION NUMBER: 60/093,491
;  EARLIER FILING DATE: 1998-07-20
;  EARLIER APPLICATION NUMBER: 60/110,941
;  EARLIER FILING DATE: 1998-12-04
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 753
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-232-195-14

  Query Match             1.7%;  Score 26;  DB 4;  Length 753;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1535 CCTACAAAAAAAAAAAAAAAAAAAAA 1560
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Db        726 CCTACAAAAAAAAAAAAAAAAAAAAA 751
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RESULT 13
US-09-261-599B-5/c
; Sequence 5, Application US/09261599B
; Patent No. 6395877
; GENERAL INFORMATION:
;  APPLICANT:  Glucksmann, Maria A.
;  TITLE OF INVENTION:  14273 Receptor, A No. 6395877el G-Protein Coupled Receptor
;  FILE REFERENCE:  5800-4B, 035800/177086
;  CURRENT APPLICATION NUMBER: US/09/261,599B
;  CURRENT FILING DATE:  1999-02-26
;  PRIOR APPLICATION NUMBER:  09/107,761
;  PRIOR FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  09/223,538
;  PRIOR FILING DATE:  1998-12-30
;  NUMBER OF SEQ ID NOS:  7
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1560
;   TYPE: DNA
;   ORGANISM: Murine ortholog
US-09-261-599B-5

  Query Match             1.7%;  Score 26;  DB 4;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAAGCTCAGCGTAAGCCTCTTCC 27
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Db        932 TGCCAAGCTCAGCGTAAGCCTCTTCC 907


RESULT 14
US-09-456-455A-5/c
; Sequence 5, Application US/09456455A
; Patent No. 6448005
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: 14273 Receptor, A No. 6448005el G-Protein Coupled Receptor
;  FILE REFERENCE: MNI-204CP3
;  CURRENT APPLICATION NUMBER: US/09/456,455A
;  CURRENT FILING DATE:  1999-12-08
;  PRIOR APPLICATION NUMBER: 09/107,761
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: 09/223,538
;  PRIOR FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
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;   TYPE: DNA
;   ORGANISM: Murine ortholog
US-09-456-455A-5

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Db        932 TGCCAAGCTCAGCGTAAGCCTCTTCC 907


RESULT 15
US-08-781-891-208
; Sequence 208, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  208:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16442 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-208

  Query Match             1.7%;  Score 26;  DB 3;  Length 16442;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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GenCore version 5.1.6

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Perfect score: 1560
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Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
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5: em_estov:*
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20: em_gss_vrt:*
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25: em_gss_rod:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	602	38.6	692	9	AV021454	AV021454 AV021454
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5	465	29.8	875	13	BU522608	BU522608 AGENCOURT
6	445	28.5	928	13	BQ936343	BQ936343 AGENCOURT
7	434	27.8	537	13	BX527210	BX527210 BX527210
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13	214	13.7	647	10	BF580577	BF580577 602097386
14	194	12.4	365	9	AA030752	AA030752 mi31h04.r
15	180	11.5	344	13	BY345055	BY345055 BY345055
16	157	10.1	377	9	AV017689	AV017689 AV017689
17	154	9.9	318	13	BY346155	BY346155 BY346155
18	154	9.9	439	9	AA647793	AA647793 vp04e04.r
19	151	9.7	315	13	BY346508	BY346508 BY346508
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c 22	112	7.2	826	14	CF587177	CF587177 AGENCOURT
23	109	7.0	265	9	AV015214	AV015214 AV015214
c 24	109	7.0	650	13	BQ256373	BQ256373 NISC_ko01
25	102	6.5	228	9	AV291417	AV291417 AV291417
c 26	102	6.5	519	10	BF454386	BF454386 maa04d01.
c 27	101	6.5	302	13	BY068200	BY068200 BY068200
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c 30	101	6.5	334	13	BY119108	BY119108 BY119108
c 31	101	6.5	336	13	BY145350	BY145350 BY145350
c 32	101	6.5	340	13	BY113754	BY113754 BY113754
c 33	101	6.5	341	13	BY117611	BY117611 BY117611
c 34	101	6.5	341	13	BY124151	BY124151 BY124151
c 35	101	6.5	344	13	BY048577	BY048577 BY048577
c 36	101	6.5	347	13	BY138060	BY138060 BY138060
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c 39	101	6.5	356	13	BY099787	BY099787 BY099787
c 40	101	6.5	359	13	BY085055	BY085055 BY085055
c 41	101	6.5	361	13	BY790047	BY790047 BY790047
c 42	101	6.5	362	13	BY106909	BY106909 BY106909
c 43	101	6.5	366	13	BY077564	BY077564 BY077564
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ALIGNMENTS

RESULT 1
AV021454
LOCUS AV021454 692 bp mRNA linear EST 23-OCT-2001
DEFINITION AV021454 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190023B03, mRNA sequence.
ACCESSION AV021454
VERSION AV021454.2 GI:16356377
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 692)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT On May 11, 1999 this sequence version replaced gi:4798446.
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

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FEATURES             Location/Qualifiers
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  Matches  602;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         89 CCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAGC 148

Qy        902 ATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTC 961
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Db        149 ATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTC 208

Qy        962 CCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCAT 1021
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Db        209 CCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCAT 268

Qy       1022 GTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCT 1081
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Db        269 GTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCT 328

Qy       1082 GGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCT 1141
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Db        329 GGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCT 388

Qy       1142 AAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTG 1201
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Db        389 AAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTG 448

Qy       1202 CTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACTT 1261
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Db        449 CTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACTT 508

Qy       1262 GTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAAG 1321
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Qy       1322 GGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCAA 1381
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Db        569 GGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCAA 628

Qy       1382 CAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTTT 1441
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Qy       1442 CC 1443
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Db        689 CC 690
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RESULT 2
AV025152

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LOCUS       AV025152                721 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  AV025152 Mus musculus adult C57BL/6J lung Mus musculus cDNA clone
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ACCESSION   AV025152
VERSION     AV025152.2  GI:15431435
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     On May 11, 1999 this sequence version replaced gi:4802144.
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
            Arakawa,T., Ishii,Y. and Hayashizaki,Y.
             Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
```

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            Func. Genomics 2 pre, L72-L86 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             35.7%;  Score 557;  DB 9;  Length 721;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  607;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        876 TCCAAAATTTTACAGATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATAC 935
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Db         61 TCCAAAATTTTACAGATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATAC 120

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Db        121 TCTGAGAGCCACCAGATCCGAGTGTCCCAACAAGACTACGGACTCTTCCGCACGCTCTTC 180

Qy        996 CTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCATCATCATCACCATCCTCCTCATC 1055
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Db        181 CTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCATCATCATCACCATCCTCCTCATC 240

Qy       1056 TTGATCCAAAACTTCCGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTG 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTGATCCAAAACTTCCGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTG 300

Qy       1116 GCCTTCACGTTTGCCAACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGG 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCCTTCACGTTTGCCAACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGG 360

Qy       1176 AACGAATGGAGGAAGATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACA 1235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACGAATGGAGGAAGATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACA 420

Qy       1236 GATACGTCTGTCAGGCGAAATGACTTGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCC 1295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATACGTCTGTCAGGCGAAATGACTTGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCC 480

Qy       1296 AGGTGAACCACGGTGTGCATGTAAAGGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCC 1355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTGAACCACGGTGTGCATGTAAAGGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCC 540

Qy       1356 CTGCTTTAAAAATACCCGACTTCCAACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAA 1415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTTTAAAAATACCCGACTTCCAACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAA 600

Qy       1416 TGATCGCTCAGTATAAAAATATTTTTCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGA 1475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGATCGCTCAGTATAAAAATATTTTTCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGA 660

Qy       1476 ACTTTTTT 1483
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Db        661 ACTTTTTT 668


RESULT 3
BQ939003
LOCUS       BQ939003                 927 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8946852 NCI_CGAP_Co24 Mus musculus cDNA clone
            IMAGE:6395027 5', mRNA sequence.
ACCESSION   BQ939003
VERSION     BQ939003.1  GI:22354481
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13889  row: a  column: 12
            High quality sequence stop: 624.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6395027"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             33.7%;  Score 525;  DB 13;  Length 927;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches  725;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
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Db         52 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 111

Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        112 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGGCTCATCTTTGTC 171

Qy        351 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 231

Qy        411 GCGTCAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 470
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GCGACAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 291

Qy        471 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 351

Qy        531 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 411

Qy        591 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 471

Qy        651 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 710
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Db        472 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 531
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Qy        711 CTCTACATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 770
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Db        532 CTCTGCATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 591

Qy        771 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAG 830
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        592 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGTG 651

Qy        831 ACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 890
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Db        652 ACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 711

Qy        891 ATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAG 950
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Db        712 ATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAG 771

Qy        951 ATCCGAGTG 959
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Db        772 ATCCGAGTG 780
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RESULT 4
BU522456
LOCUS BU522456 870 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10153856 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6528871 5', mRNA sequence.
ACCESSION BU522456
VERSION BU522456.1 GI:22829982
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14128 row: b column: 07
High quality sequence stop: 615.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6528871"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match            30.8%;  Score 481;  DB 13;  Length 870;
  Best Local Similarity  99.4%;  Pred. No. 0;
  Matches  681;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 107

Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        108 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGGCTCATCTTTGTC 167

Qy        351 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 227

Qy        411 GCGTCAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 470
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Db        228 GCGACAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 287

Qy        471 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 347

Qy        531 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 407

Qy        591 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 650
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Db        408 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 467

Qy        651 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 710
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Db        468 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 527

Qy        711 CTCTACATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 770
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Db        528 CTCTGCATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 587

Qy        771 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAG 830
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        588 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGTG 647

Qy        831 ACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 890
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Db        648 ACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 707

Qy        891 ATCACGAAAGCATCGCGGAAGAGGC 915
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Db        708 ATCACGAAAGCATCGCGGAAGAGGC 732
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RESULT 5
BU522608
LOCUS BU522608 875 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10154009 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6529120 5', mRNA sequence.
ACCESSION BU522608
VERSION BU522608.1 GI:22830134
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14128 row: l column: 16
High quality sequence stop: 653.

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FEATURES             Location/Qualifiers
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                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6529120"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match            29.8%;  Score 465;  DB 13;  Length 875;
  Best Local Similarity  99.4%;  Pred. No. 0;
  Matches  665;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
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Db         84 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 143

Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
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Db        144 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGGCTCATCTTTGTC 203

Qy        351 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 410
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Db        204 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 263

Qy        411 GCGTCAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 470
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GCGACAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 323

Qy        471 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 530
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Db        324 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 383

Qy        531 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 590
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Db        384 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 443

Qy        591 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 503

Qy        651 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 563

Qy        711 CTCTACATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 770
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CTCTGCATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 623

Qy        771 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAG 830
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Db        624 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGTG 683

Qy        831 ACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 890
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Db        684 ACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 743

Qy        891 ATCACGAAA 899
              |||||||||
Db        744 ATCACGAAA 752


RESULT 6
BQ936343
LOCUS       BQ936343                928 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_10013769 NCI_CGAP_Mam2 Mus musculus cDNA clone
            IMAGE:6488067 5', mRNA sequence.
ACCESSION   BQ936343
VERSION     BQ936343.1  GI:22351726
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14034  row: b  column: 04
            High quality sequence stop: 605.
FEATURES             Location/Qualifiers
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                     /strain="FVB/N-3"
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                     /clone="IMAGE:6488067"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam2"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match            28.5%;  Score 445;  DB 13;  Length 928;
  Best Local Similarity  99.5%;  Pred. No. 0;
  Matches  595;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
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Db         69 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 128

Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
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Qy        351 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 410
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Db        189 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 248

Qy        411 GCGTCAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 470
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Db        249 GCGACAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 308

Qy        471 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 530
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Db        309 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 368

Qy        531 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 590
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Db        369 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 428

Qy        591 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 488

Qy        651 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 548
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Qy        711 CTCTACATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 770
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTCTGCATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 608

Qy        771 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTG 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTG 666


RESULT 7
BX527210
LOCUS       BX527210                537 bp    mRNA    linear   EST 27-JUN-2003
DEFINITION  BX527210 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
            IMAGp998K072670 ; IMAGE:1067646, mRNA sequence.
ACCESSION   BX527210
VERSION     BX527210.1  GI:32304990
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 537)
  AUTHORS   Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
            and Korn,B.
  TITLE     Mouse UnigeneSet - RZPD2
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998K072670.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            T7, Primer sequence: TAATACGACTCACTATAGGG.
FEATURES              Location/Qualifiers
     source           1. .537
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="IMAGp998K072670 ; IMAGE:1067646"
                      /sex="male"
                      /tissue_type="mammary gland"
                      /dev_stage="4 weeks"
                      /lab_host="DH10B"
                      /clone_lib="Soares_mammary_gland_NbMMG"
                      /note="Organ: mammary gland; Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                      oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI
                      adaptors (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of the modified pT7T3 vector.
                      RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                      constructed and normalized by Bento Soares and M.Fatima
                      Bonaldo."
ORIGIN

  Query Match             27.8%;  Score 434;  DB 13;  Length 537;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  534;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        561 AGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCGC 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          2 AGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCGC 61

Qy        621 CTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGGCGGCACTGCTGGCTTTCATA 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGGCGGCACTGCTGGCTTTCATA 121

Qy        681 TGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCTTGTTCCGCGTGGTCCCGCAG 740
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        122 TGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTGCATCTTGTTCCGCGTGGTCCCGCAG 181

Qy        741 CGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACATTGGATTGGCCCAACCGCATA 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACATTGGATTGGCCCAACCGCATA 241

Qy        801 GGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACTTCCTGGTGCCGGGACTGGTC 860
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        242 GGAGAAATCTCATGGGATGTGTTTTTTGTGACTTTGAACTTCCTGGTGCCGGGACTGGTC 301

Qy        861 ATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAGCATCGCGGAAGAGGCTTACG 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAGCATCGCGGAAGAGGCTTACG 361

Qy        921 CTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAAGACTACCGACTC 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAAGACTACCGACTC 421

Qy        981 TTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCATCATCATC 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 TTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCATCATCATC 481

Qy       1041 ACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGGTCATCTGGCCATC 1096
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Db        482 ACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGGTCATCTGGCCATC 537


RESULT 8
BB609925
LOCUS       BB609925                671 bp    mRNA    linear   EST 31-AUG-2001
DEFINITION  BB609925 RIKEN full-length enriched, adult male lung Mus musculus
            cDNA clone 1200010P16 5', mRNA sequence.
ACCESSION   BB609925
VERSION     BB609925.1  GI:15390516
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 671)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
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Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

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FEATURES             Location/Qualifiers
     source          1. .671
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="1200010P16"
                     /sex="male"
                     /tissue_type="lung"
                     /dev_stage="adult"
                     /lab_host="SOLR"
                     /clone_lib="RIKEN full-length enriched, adult male lung"
                     /note="Site_1: XhoI; Site_2: SstI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTAATTAAACCCCCCCCCCC 3'].
                     cDNA was cleaved with XhoI and SstI."
ORIGIN

  Query Match             26.9%;  Score 420;  DB 10;  Length 671;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches  570;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 142

Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        143 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGGCTCATCTTTGTC 202

Qy        351 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 262

Qy        411 GCGTCAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 470
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Db        263 GCGACAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 322

Qy        471 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 382

Qy        531 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 442

Qy        591 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 502

Qy        651 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 562

Qy        711 CTCTACATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 770
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CTCTGCATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 622

Qy        771 ATTTGCACATTGGATTGGCCCAACCGCATAGGA 803
              |||||||||||||||||||||||||||||||||
Db        623 ATTTGCACATTGGATTGGCCCAACCGCATAGGA 655
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RESULT 9
CG557110
LOCUS       CG557110                517 bp    DNA     linear   GSS 01-OCT-2003
DEFINITION  OST173216 Mus musculus 129Sv/Ev Mus musculus genomic clone
            OST173216, genomic survey sequence.
ACCESSION   CG557110
VERSION     CG557110.1  GI:37343697
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
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                     /strain="129SV/EV"
                     /db_xref="taxon:10090"
                     /clone="OST173216"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             26.2%;  Score 408;  DB 29;  Length 517;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  408;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        830 GACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACA 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACA 135

Qy        890 GATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCA 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCA 195

Qy        950 GATCCGAGTGTCCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTC 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        196 GATCCGAGTGTCCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTC 255

Qy       1010 CTTCTTCATCATGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTT 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 CTTCTTCATCATGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTT 315

Qy       1070 CCGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGC 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CCGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGC 375

Qy       1130 CAACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAA 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 CAACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAA 435

Qy       1190 GATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGA 1237
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGA 483


RESULT 10
BB609814
LOCUS       BB609814                637 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB609814 RIKEN full-length enriched, 18 days embryo Mus musculus
            cDNA clone 1190023B03 5', mRNA sequence.
ACCESSION   BB609814
VERSION     BB609814.1  GI:16451529
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .637
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                     /lab_host="SOLR"
                     /clone_lib="RIKEN full-length enriched, 18 days embryo"
                     /note="Site_1: XhoI; Site_2: SstI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTAATTAAACCCCCCCCCCC 3'].
                     cDNA was cleaved with XhoI and SstI."
ORIGIN

  Query Match             24.5%;  Score 382;  DB 10;  Length 637;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  482;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
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Db         68 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 127

Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        128 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGGCTCATCTTTGTC 187

Qy        351 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 GTCTCACTGCTGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGG 247

Qy        411 GCGTCAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 470
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GCGACAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 307

Qy        471 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 367

Qy        531 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 427

Qy        591 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 487

Qy        651 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 547

Qy        711 CTCT 714
              ||||
Db        548 CTCT 551


RESULT 11
AI552415/c
LOCUS       AI552415                437 bp    mRNA    linear   EST 23-MAR-1999
DEFINITION  vp04e04.x1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
            IMAGE:1067646 3', mRNA sequence.
```

```
ACCESSION   AI552415
VERSION     AI552415.1  GI:4484778
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:590006
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end
            High quality sequence stop: 399.
FEATURES             Location/Qualifiers
     source          1. .437
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1067646"
                     /sex="male"
                     /tissue_type="mammary gland"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_mammary_gland_NbMMG"
                     /note="Organ: mammary gland; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
ORIGIN

  Query Match           17.8%;  Score 278;  DB 9;  Length 437;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches  378;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1104 TTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCTAAACCCCATACTGTACAACATG 1163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 TTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCTAAACCCCATACTGTACAACATG 378

Qy       1164 TCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGA 1223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 TCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGA 318

Qy       1224 GCCATTTTTACAGATACGTCTGTCAGGCGAAATGACTTGTCTGTTATTTCCAGCTAACTA 1283
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GCCATTTTTACAGACACGTCTGTCAGGCGAAATGACTTGTCTGTTATTTCCAGCTAACTA 258

Qy       1284 GCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAAGGGAGTTAACTTCAAGGAAAGCC 1343
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        257 GCCTCTGGTGCTAGGTGAACCACGGTGTGCATGTAAAGGGAGTTAACTTCAAGGAAAGCC 198

Qy       1344 CACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCAACAGCAGGCATCTACGGAGCCAG 1403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 CACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCAACAGCAGGCATCTACGGAGCCAG 138

Qy       1404 CAAATTAAGGAATGATCGCTCAGTATAAAAATATTTTTCCTTAAAAGAACTTTCTATGGG 1463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CAAATTAAGGAATGATCGCTCAGTATAAAAATATTTTTCCTTAAAAGAACTTTCTATGGG 78

Qy       1464 TTCCTTTTGTGAACTTTTTT 1483
              ||||||||||||||||||||
Db          77 TTCCTTTTGTGAACTTTTTT 58


RESULT 12
CG617050
LOCUS       CG617050                492 bp    DNA     linear   GSS 02-OCT-2003
DEFINITION  OST310062 Mus musculus 129Sv/Ev Mus musculus genomic clone
            OST310062, genomic survey sequence.
ACCESSION   CG617050
VERSION     CG617050.1  GI:37440899
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 492)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .492
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129SV/EV"
                     /db_xref="taxon:10090"
                     /clone="OST310062"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match           17.2%;  Score 269;  DB 29;  Length 492;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  269;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        969 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 232

Qy       1029 CCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGGTCATC 1088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 CCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGGTCATC 292

Qy       1089 TGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCTAAACCCC 1148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCTAAACCCC 352

Qy       1149 ATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTGCTTCTTT 1208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 ATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTGCTTCTTT 412

Qy       1209 TTTCCAGAGAAGGGAGCCATTTTTACAGA 1237
              |||||||||||||||||||||||||||||
Db        413 TTTCCAGAGAAGGGAGCCATTTTTACAGA 441


RESULT 13
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```
BF580577
LOCUS       BF580577                 647 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602097386F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4217252 5',
            mRNA sequence.
ACCESSION   BF580577
VERSION     BF580577.1  GI:11654289
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 647)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9795  row: 1  column: 21
            High quality sequence stop: 626.
FEATURES             Location/Qualifiers
     source          1. .647
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4217252"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match            13.7%;  Score 214;  DB 10;  Length 647;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        913 GGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAAGACT 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAAGACT 60

Qy        973 ACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCA 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCA 120

Qy       1033 TCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGGTCATCTGGC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGGTCATCTGGC 180

Qy       1093 CATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTT 1126
              |||||||||||||||||||||||||||||||||
Db        181 CATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTT 214


RESULT 14
AA030752
LOCUS       AA030752                 365 bp    mRNA    linear   EST 21-AUG-1996
DEFINITION  mi31h04.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
            clone IMAGE:465175 5', mRNA sequence.
ACCESSION   AA030752
VERSION     AA030752.1  GI:1500749
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 365)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:278991
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .365
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:465175"
                     /sex="unknown"
                     /tissue_type="embryo"
                     /dev_stage="13.5-14.5dpc total fetus"
                     /lab_host="DH10B"
                     /clone_lib="Soares mouse embryo NbME13.5 14.5"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTT
                     T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                     14.5dpc embryos [total RNA provided by  Minoru Ko, Wayne
                     State Univ., from 2 ]; double-stranded cDNA was ligated to
                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector. Library went through one round of
                     normalization, and was constructed by Bento Soares and
                     M.Fatima Bonaldo.  "
ORIGIN

  Query Match            12.4%;  Score 194;  DB 9;  Length 365;
  Best Local Similarity  99.5%;  Pred. No. 0;
  Matches  364;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy        904 CGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCC 963
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCC 60

Qy        964 AACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGT 1023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGT 120

Qy       1024 GGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGG 1083
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 GGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCA-GACCTGG 179

Qy       1084 TCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCTAA 1143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 TCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCTAA 239

Qy       1144 ACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTGCT 1203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 ACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTGCT 299

Qy       1204 TCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACTTGT 1263
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        300 TCTGTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACTTGT 359

Qy       1264 CTGTTA 1269
              ||||||
Db        360 CTGTTA 365


RESULT 15
BY345055
LOCUS       BY345055                344 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  BY345055 RIKEN full-length enriched, whole joints Mus musculus cDNA
            clone L730011C21 5', mRNA sequence.
ACCESSION   BY345055
VERSION     BY345055.1  GI:26574543
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 344)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
            Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
            Fleming street 16672 Vari,Greece ) whose assistance we gratefully
            acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .344
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="L730011C21"
                     /tissue_type="whole joints"
                     /clone_lib="RIKEN full-length enriched, whole joints"
ORIGIN

  Query Match             11.5%;  Score 180;  DB 13;  Length 344;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches  280;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 122

Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
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Db        123 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGGCTCATCTTTGTC 182

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 19:03:02 ; Search time 6615.8 Seconds
(without alignments)
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Title: US-10-077-698-2
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	693	39.8	744	9	AY255573	AY255573 Homo sapi
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16	298	17.1	760	6	BD129472	BD129472 Human gen
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ALIGNMENTS

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LOCUS BD240720 1743 bp DNA linear PAT 17-JUL-2003
DEFINITION 14273 receptor, a G-protein coupled receptor.
ACCESSION BD240720
VERSION BD240720.1 GI:33050490
KEYWORDS JP 2002522011-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1743)
AUTHORS Glucksmann,M.A. and Tsai,F.Y.
TITLE 14273 receptor, a G-protein coupled receptor
JOURNAL Patent: JP 2002522011-A 1 23-JUL-2002;

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            MILLENNIUM PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002522011-A/1
            PD   23-JUL-2002
            PF   30-JUN-1999 JP 2000557364
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            26-FEB-1999 US    09/261599
            PI   MARIA ALEXANDRA GLUCKSMANN,FONG YING TSAI
            PC   C12N15/09,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
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DEFINITION  14273 receptor, a novel G-protein coupled receptor.
ACCESSION   BD269630
VERSION     BD269630.1  GI:33079398
KEYWORDS    JP 2002536997-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1743)
  AUTHORS   Glucksmann,M.A. and Tsai,F.Y.
  TITLE     14273 receptor, a novel G-protein coupled receptor
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COMMENT     OS   Homo sapiens (human)
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            PD   05-NOV-2002
            PF   28-FEB-2000 JP 2000601160
            PR   26-FEB-1999 US    09/261599,08-DEC-1999 US    09/456455 PI
            MARIA ALEXANDRA GLUCKSMANN,FONG YING TSAI
            PC   C12N15/09,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
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Db        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960

Qy        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
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Db        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020

Qy       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
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Db       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080

Qy       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
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Db       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140

Qy       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
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Db       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200

Qy       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260

Qy       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
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Db       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380

Qy       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
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Db       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440

Qy       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
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Db       1441 TACTAAAAATAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500

Qy       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560
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Db       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560

Qy       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620
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Db       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620

Qy       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680
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Db       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680

Qy       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAAGGG 1740
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Db       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAAGGG 1740

Qy       1741 CGG 1743
             |||
Db       1741 CGG 1743


RESULT 3
AR228216
LOCUS       AR228216               1743 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6448005.
ACCESSION   AR228216
VERSION     AR228216.1  GI:27266963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1743)
  AUTHORS   Glucksmann,M.A. and Tsai,F.-Y.
  TITLE     14723 Receptor, a novel G-protein coupled receptor
  JOURNAL   Patent: US 6448005-A 2 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .1743
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1743;  DB 6;  Length 1743;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1743;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60

Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120

Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
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Db        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180

Qy        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240
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Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
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Db        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300

Qy        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
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Db        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360

Qy        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
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Db        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420

Qy        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480
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Db        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480

Qy        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
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Db        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540

Qy        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600
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Db        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600

Qy        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660
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Db        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660

Qy        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720

Qy        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780
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Db        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780

Qy        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840
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Db        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840

Qy        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900
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Db        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
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Qy        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
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Db        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020

Qy       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080

Qy       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
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Qy       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
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Qy       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
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Db       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260

Qy       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
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Db       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
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Qy       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
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Qy       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
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Qy       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560
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Db       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560

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Qy       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680
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Db       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680

Qy       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAAGGG 1740
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Db       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAAGGG 1740

Qy       1741 CGG 1743
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Db       1741 CGG 1743


RESULT 4
AR372101
LOCUS       AR372101                1743 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 2 from patent US 6395877.
ACCESSION   AR372101
VERSION     AR372101.1  GI:34609378
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1743)
  AUTHORS   Glucksmann,M.A. and Tsai,F.-Y.
  TITLE     14273 receptor, a novel G-protein coupled receptor
  JOURNAL   Patent: US 6395877-A 2 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .1743
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 1743;  DB 6;  Length 1743;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1743;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60

Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
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Db         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120

Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
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Db        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180

Qy        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240
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Db        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240

Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
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Db        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300

Qy        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360

Qy        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420

Qy        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480
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Db        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480

Qy        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540

Qy        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600
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Qy        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660
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Db        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660

Qy        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720

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Db        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780

Qy        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840

Qy        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900
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Db        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960

Qy        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020

Qy       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080

Qy       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140

Qy       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
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Qy       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
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Qy       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
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Db       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
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Qy       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
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Db       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440

Qy       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
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Db       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500

Qy       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560
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Qy       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620
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Db       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680

Qy       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740
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Db       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740

Qy       1741 CGG 1743
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Db       1741 CGG 1743
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RESULT 5
BD015337
LOCUS BD015337 1458 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel polypeptide.
ACCESSION BD015337
VERSION BD015337.1 GI:22556475
KEYWORDS JP 2001211885-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1458)
AUTHORS Yoshimatsu,H., Sasaki,K., Nakatani,Y., Saeki,S., Miura,K. and Sekine,S.
TITLE Novel polypeptide
JOURNAL Patent: JP 2001211885-A 1 07-AUG-2001;
KYOWA HAKKO KOGYO CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2001211885-A/1
PD 07-AUG-2001
PF 02-FEB-2000 JP 2000024921
PI HAJIME YOSHIMATSU,KATSUTOSHI SASAKI,YUKIE NAKATANI,SATOSHI PI SAEKI,
PI KAZUMI MIURA,SUSUMU SEKINE
PC C12N15/09,A01H5/00,A01K67/027,A61K38/00,A61K39/395,A61K39/395, PC A61K39/395,
PC A61K45/00,A61P5/08,A61P35/00,C07K14/705,C07K16/28,C12N1/15, PC C12N1/19,
PC C12N1/21,C12N5/10,C12N5/10,C12P21/02,C12P21/08,C12Q1/68 PC ,C12Q1/68,G01N33/15,
PC G01N33/50,G01N33/566,C12N15/00,A61K37/02,C12N5/00,C12N5/00 CC
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1. .1458
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 76.2%; Score 1328; DB 6; Length 1458;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         15 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 74
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Db         29 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 88

Qy         75 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 134
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Db         89 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 148

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Qy        255 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 314
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Qy        375 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCG 434
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Qy        555 TGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAA 614
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Qy        615 TTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTT 674
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Db        629 TTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTT 688

Qy        675 TTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTT 734
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Db        689 TTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTT 748

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Db        749 TACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCC 808

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Db        869 TCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGA 928

Qy        915 ACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACAT 974
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Qy       1035 AGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTG 1094
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Qy       1095 TCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCA 1154
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Db       1109 TCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCA 1168

Qy       1155 CACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTG 1214
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Db       1169 CACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTG 1228

Qy       1215 CACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAG 1274
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Db       1229 CACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAG 1288

Qy       1275 GGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCA 1334
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Db    1289 GGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCA 1348

Qy    1335 GTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGT 1394
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Db    1349 GTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGT 1408

Qy    1395 CAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCGTCTCTACT 1444
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Db    1409 CAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCGTCTCTACT 1458


RESULT 6
AX168141
LOCUS       AX168141                1321 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 59 from Patent WO0142288.
ACCESSION   AX168141
VERSION     AX168141.1  GI:14597419
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burford,N., Baughn,M.R., Au-Young,J., Yang,J., Lu,D.A. and Reddy,R.
  TITLE     G-protein coupled receptors
  JOURNAL   Patent: WO 0142288-A 59 14-JUN-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             62.0%;  Score 1081;  DB 6;  Length 1321;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1181;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy     332 GCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTAC 391
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Qy     392 GTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGC 451
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Db     378 GTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGC 437

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Db     438 ATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCA 497

Qy     512 GTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTC 571
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Qy     632 ATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTC 691
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Qy     692 TTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCA 751
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Qy     812 CAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATG 871
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Qy     872 TGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTG 931
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Db     858 TGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTG 917

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Db     918 GTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTA 977

Qy     992 AACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGC 1051
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Db     978 AACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGC 1037

Qy    1052 TTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTG 1111
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Db    1098 TCGATTATTTCTGGCTAATTTTTCTTTATAGCAGAGTTTCTCACACCTGGCGAGCTGTGG 1157

Qy    1172 CATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTG 1214
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Db    1158 CATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTG 1200


RESULT 7
AL356214
LOCUS       AL356214              163964 bp    DNA     linear   PRI 13-APR-2001
DEFINITION  Human DNA sequence from clone RP11-30E16 on chromosome 10, complete
            sequence.
ACCESSION   AL356214
VERSION     AL356214.20  GI:13624997
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 163964)
  AUTHORS   Brown,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Apr 14, 2001 this sequence version replaced gi:13160256.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
```

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
RP11-30E16 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-30E16 The true left end of clone RP11-437J2 is at 129920 in this sequence. The true right end of clone RP11-313N18 is at 82571 in this sequence.

FEATURES Location/Qualifiers

source	1. .163964	/organism="Homo sapiens"
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repeat_region	197. .317	/note="L1ME3A repeat: matches 5968. .6084 of consensus"
repeat_region	318. .613	/note="AluSq repeat: matches 1. .299 of consensus"
repeat_region	819. .977	/note="L1ME3A repeat: matches 5793. .5946 of consensus"
repeat_region	978. .1278	/note="AluSg repeat: matches 1. .301 of consensus"
repeat_region	1279. .1632	/note="L1ME3A repeat: matches 5417. .5793 of consensus"
repeat_region	1742. .2022	/note="AluJb repeat: matches 3. .302 of consensus"
repeat_region	2038. .2170	/note="FLAM_A repeat: matches 8. .140 of consensus"
repeat_region	2289. .2593	/note="L1ME repeat: matches 5232. .5552 of consensus"
repeat_region	2600. .2898	/note="L1M4 repeat: matches 3953. .4253 of consensus"
repeat_region	2907. .3078	/note="FAM repeat: matches -122. .49 of consensus"
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repeat_region	3867. .4138	/note="AluJo repeat: matches 6. .290 of consensus"
repeat_region	4154. .4598	/note="HAL1 repeat: matches 1183. .1645 of consensus"
repeat_region	4599. .4907	/note="AluJb repeat: matches 1. .312 of consensus"
repeat_region	4908. .4997	/note="HAL1 repeat: matches 1097. .1183 of consensus"
repeat_region	5083. .5298	/note="HAL1 repeat: matches 695. .969 of consensus"
repeat_region	5467. .5734	/note="LTR16A repeat: matches 18. .283 of consensus"
repeat_region	5868. .5952	/note="HERV16 repeat: matches 4. .92 of consensus"
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repeat_region	8566. .8718	/note="FLAM_C repeat: matches 1. .133 of consensus"
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repeat_region	9424. .9511	/note="L2 repeat: matches 2317. .2412 of consensus"
repeat_region	9752. .10112	/note="Charlie5 repeat: matches 2210. .2585 of consensus"
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misc_feature	12527. .13073	/note="CpG island"
		/evidence=not_experimental
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repeat_region	14293. .14330	/note="19 copies 2 mer aa 81% conserved"
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repeat_region	15669. .15969	/note="AluSg repeat: matches 1. .301 of consensus"
repeat_region	16912. .17073	/note="FRAM repeat: matches 1. .161 of consensus"
repeat_region	17557. .17845	/note="AluSx repeat: matches 1. .310 of consensus"
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repeat_region	21583. .21657	/note="MLT1J repeat: matches 113. .200 of consensus"
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     repeat_region   27088. .27386
                     /note="AluSg repeat: matches 3. .299 of consensus"
     repeat_region   27741. .28051
                     /note="AluSg repeat: matches 1. .300 of consensus"
     repeat_region   28061. .28094
                     /note="17 copies 2 mer aa 82% conserved"
     repeat_region   28102. .28390
                     /note="AluSx repeat: matches 6. .296 of consensus"
     repeat_region   28393. .28687
                     /note="AluSq repeat: matches 1. .306 of consensus"
     repeat_region   29954. .30100
                     /note="MLT1C repeat: matches 82. .231 of consensus"
     repeat_region   30101. .30380
                     /note="AluSx repeat: matches 1. .294 of consensus"
     repeat_region   30381. .30458
                     /note="MLT1C repeat: matches 6. .83 of consensus"
     repeat_region   30573. .30709
                     /note="LTR16B repeat: matches 319. .462 of consensus"
     repeat_region   30919. .31222
                     /note="AluSq repeat: matches 1. .305 of consensus"
     repeat_region   31234. .31279
                     /note="LTR16A repeat: matches 1. .45 of consensus"
     repeat_region   32166. .32272
                     /note="MIR repeat: matches 124. .228 of consensus"
     repeat_region   32606. .32639
                     /note="17 copies 2 mer tc 88% conserved"
     repeat_region   33420. .33763
                     /note="L2 repeat: matches 2325. .2742 of consensus"
     repeat_region   34296. .34599

  Query Match           56.6%;  Score 986;  DB 9;  Length 163964;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        736 ACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCCA 795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103366 ACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCCA 103425

Qy        796 CCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGT 855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103426 CCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGT 103485

Qy        856 CTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAA 915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103486 CTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAA 103545

Qy        916 CTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATT 975
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Db     103546 CTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATT 103605

Qy        976 TGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAA 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103606 TGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAA 103665

Qy       1036 GAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGT 1095
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Db     103666 GAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGT 103725

Qy       1096 CAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCAC 1155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103726 CAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCAC 103785

Qy       1156 ACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTGC 1215
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Db     103786 ACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTGC 103845

Qy       1216 ACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAGG 1275
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Db     103846 ACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAGG 103905

Qy       1276 GGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCAG 1335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103906 GGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCAG 103965

Qy       1336 TGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTC 1395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103966 TGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTC 104025

Qy       1396 AGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTCTACTAAAAATAAAAA 1455
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Db     104026 AGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTCTACTAAAAATAAAAA 104085

Qy       1456 AAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTACTTGGGAGGCTGAAC 1515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     104086 AAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTACTTGGGAGGCTGAAC 104145

Qy       1516 CAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGC 1575
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Db     104146 CAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGC 104205

Qy       1576 ACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAAAAAAAAAAAGATTTGT 1635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     104206 ACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAAAAAAAAAAAGATTTGT 104265

Qy       1636 TATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATATGATCAAATTTAATA 1695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     104266 TATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATATGATCAAATTTAATA 104325

Qy       1696 AATATTTATTTATGACTGTTCAGCAA 1721
              |||||||||||||||||||||||||
Db     104326 AATATTTATTTATGACTGTTCAGCAA 104351

RESULT 8
AX498184
LOCUS       AX498184                1086 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 7 from Patent WO0242461.
ACCESSION   AX498184
VERSION     AX498184.1  GI:23343113
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,R., Chu,Z.L., Dang,H.T., Lowitz,K.P. and Pride,C.
  TITLE     Endogenous and non-endogenous versions of human g protein-coupled
            receptors
  JOURNAL   Patent: WO 0242461-A 7 30-MAY-2002;
            Arena Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1086
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Novel Sequence"
ORIGIN

  Query Match           53.1%;  Score 926;  DB 6;  Length 1086;
  Best Local Similarity  99.7%;  Pred. No. 0;
  Matches 1076;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 CTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCA 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCA 67

Qy        111 CCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGG 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 CCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGG 127

Qy        171 AGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGG 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGG 187

Qy        231 TGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCT 290
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Db        188 TGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCT 247

Qy        291 GCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGG 307

Qy        351 CCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCA 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCA 367

Qy        411 GCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACC 427

Qy        471 TGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        428 TGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATAT 487

Qy        531 GGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAAC 590
              |||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||
Db        488 GGGGCTATTCGGCGGTCGCCGCTCTGCCTCTATGCGTCTTCTTCCGAGTCGTCCCGCAAC 547

Qy        591 GGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 GGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTG 607

Qy        651 GAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCA 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCA 667

Qy        711 TTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGG 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 TTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGG 727

Qy        771 TAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCT 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 TAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCT 787

Qy        831 TCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCA 890
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Db        788 TCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCA 847

Qy        891 CCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCT 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 CCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCT 907

Qy        951 TCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACA 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 TCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACA 967

Qy       1011 TGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGG 1070
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Db        968 TGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGG 1027

Qy       1071 GAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAA 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 GAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAA 1086


RESULT 9
AY255573
LOCUS       AY255573                744 bp    mRNA    linear   PRI 08-APR-2003
DEFINITION  Homo sapiens G protein-coupled receptor PGR4 mRNA, partial cds.
ACCESSION   AY255573
VERSION     AY255573.1  GI:29611547
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 744)
  AUTHORS   Vassilatis,D.K., Hohmann,J.G., Zeng,H., Li,F., Ranchalis,J.E.,
            Mortrud,M.T., Brown,A., Rodriguez,S.S., Weller,J.R., Wright,A.C.,
            Bergmann,J.E. and Gaitanaris,G.A.
  TITLE     The G Protein-Coupled Receptor Repertoires of Human and Mouse
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (8), 4903-4908 (2003)
REFERENCE   2  (bases 1 to 744)
  AUTHORS   Vassilatis,D.K., Hohmann,J.G., Zeng,H., Li,F., Ranchalis,J.E.,
            Mortrud,M.T., Brown,A., Rodriguez,S.S., Weller,J.R., Wright,A.C.,
            Bergmann,J.E. and Gaitanaris,G.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-2003) Primal, Inc., 1124 Columbia Street,
            Seattle, WA 98104, USA
FEATURES             Location/Qualifiers
     source          1. .744
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             <1. .>744
                     /note="similar to NPY2R"
                     /codon_start=1
                     /product="G protein-coupled receptor PGR4"
                     /protein_id="AAO85085.1"
                     /db_xref="GI:29611548"
                     /translation="LIFAVSLLGNVCALVLVARRRRRGATACLVLNLFCADLLFISAI
                     PLVLAVRWTEAWLLGPVACHLLFYVMTLSGSVTILTLAAVSLERMVCIVHLQRGVRGP
                     GRRARAVLLALIWGYSAVAALPLCVFFRVVPQRLPGADQEISICTLIWPTIPGEISWD
                     VSFVTLNFLVPGLVIVISYSKILQITKASRKRLTVSLAYSESHQIRVSQQDFRLFRTL
                     FLLMVSFFIMWSPIIITILLILIQNFKQDL"
ORIGIN

  Query Match           39.8%;  Score 693;  DB 9;  Length 744;
  Best Local Similarity 99.9%;  Pred. No. 0;
  Matches  743;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        188 CTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGA 60

Qy        248 CGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTC 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTC 120

Qy        308 ATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCC 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCC 180

Qy        368 GTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACG 427
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Db        181 GTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACG 240

Qy        428 CTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGG 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGG 300

Qy        488 GGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTC 547
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Db        301 GGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTC 360

Qy        548 GCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGAC 607
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        361 GCCGCTCTGCCTCTCTGCGTCTTCTTCCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGAC 420

Qy        608 CAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGAT 667
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Db        421 CAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGAT 480

Qy        668 GTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCC 727
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Db        481 GTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCC 540

Qy        728 AAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCG 787
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Db        541 AAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCG 600
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Qy        788 GAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTC 847
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Db        601 GAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTC 660

Qy        848 CTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTG 907
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Db        661 CTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTG 720

Qy        908 ATCCAGAACTTCAAGCAAGACCTG 931
              |||||||||||||||||||||||
Db        721 ATCCAGAACTTCAAGCAAGACCTG 744


RESULT 10
AX647273
LOCUS       AX647273               1066 bp    DNA     linear   PAT 04-MAR-2003
DEFINITION  Sequence 1465 from Patent EP1270724.
ACCESSION   AX647273
VERSION     AX647273.1  GI:28800736
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.
  TITLE     Guanosine triphosphate-binding protein coupled receptors
  JOURNAL   Patent: EP 1270724-A 1465 02-JAN-2003;
            National Institute of Advanced Industrial Science and Technology
            (JP) ; Center for Advanced Science and Technology Incubation, Ltd.
            (JP)
FEATURES             Location/Qualifiers
     source          1. .1066
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                     /db_xref="taxon:9606"
     CDS             201. .866
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                     /codon_start=1
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                     /db_xref="GI:28800737"
                     /db_xref="REMTREMBL:CAD69757"
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                     EQQ"
ORIGIN

  Query Match           32.1%;  Score 559;  DB 6;  Length 1066;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-313;
  Matches  559;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 74
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Db        172 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 231

Qy         75 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 134
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Db        232 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 291

Qy        135 TCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCT 194
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Db        292 TCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCT 351

Qy        195 TTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCC 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCC 411

Qy        255 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 314
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Db        412 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 471

Qy        315 CTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCT 374
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Db        472 CTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCT 531

Qy        375 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCG 434
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Db        532 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCG 591

Qy        435 CGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTG 494
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Db        592 CGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTG 651

Qy        495 GGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTC 711

Qy        555 TGCCTCTCTGCGTCTTCTT 573
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Db        712 TGCCTCTCTGCGTCTTCTT 730


RESULT 11
AY288417
LOCUS       AY288417               1131 bp    mRNA    linear   PRI 08-DEC-2003
DEFINITION  Homo sapiens G protein-coupled receptor 120 (GPR120) mRNA, complete
            cds.
ACCESSION   AY288417
VERSION     AY288417.1  GI:32165517
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1131)
  AUTHORS   Fredriksson,R., Hoglund,P.J., Gloriam,D.E., Lagerstrom,M.C. and
            Schioth,H.B.
  TITLE     Seven evolutionarily conserved human rhodopsin G protein-coupled
            receptors lacking close relatives
  JOURNAL   FEBS Lett. 554 (3), 381-388 (2003)
  MEDLINE   22985413
   PUBMED   14623098
REFERENCE   2  (bases 1 to 1131)
  AUTHORS   Fredriksson,R., Hoglund,P.J., Gloriam,D.E.I., Lagerstrom,M.C. and
            Schioth,H.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-2003) Neuroscience; Unit of Pharmacology, Uppsala
            University, Box 593, Uppsala 75124, Sweden
FEATURES             Location/Qualifiers
     source          1. .1131
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1. .1131
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     CDS             1. .1131
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                     /protein_id="AAP72126.1"
                     /db_xref="GI:32165518"
                     /translation="MSPECARAAGDAPLRSLEQANRTRFPPFFSDVKGDHRLVLAAVET
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                     IWGYSAVAALPLCVFFRVVPQRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVP
                     GLVIVISYSKILQTSEHLLDARAVVTHSEITKASRKRLTVSLAYSESHQIRVSQQDFR
                     LFRTLFLLMVSFFIMWSPIIITILLILIQNFKQDLVIWPSLFFWVVAFTFANSALNPI
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ORIGIN

  Query Match           25.5%;  Score 445;  DB 9;  Length 1131;
  Best Local Similarity  99.8%;  Pred. No. 7.6e-247;
  Matches  495;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy        245 CGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTC 304
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Db        199 CGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTC 258

Qy        305 TTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGC 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 TTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGC 318

Qy        365 CCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTC 378

Qy        425 ACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTG 484
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Db        379 ACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTG 438

Qy        485 CGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCG 544
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Db        439 CGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCG 498

Qy        545 GTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCC 604
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        499 GTCGCCGCTCTGCCTCTCTGCGTCTTCTTCCGAGTCGTCCCGCAACGGCTCCCCGGCGCC 558

Qy        605 GACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGG 664
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Db        559 GACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGG 618

Qy        665 GATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTAC 724
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Db        619 GATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTAC 678

Qy        725 TCCAAAATTTTACAGA 740
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Db        679 TCCAAAATTTTACAGA 694
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RESULT 12
AX657504
LOCUS AX657504 933 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 87 from Patent WO03000893.
ACCESSION AX657504
VERSION AX657504.1 GI:29160243
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Martinez,R.M. and Sigurdsson,G.T.
TITLE Nucleic acids encoding G protein-coupled receptors
JOURNAL Patent: WO 03000893-A 87 03-JAN-2003;
Decode Genetics EHF. (IS)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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CDS <1. .>933
/note="unnamed protein product"
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/db_xref="REMTREMBL:CAD79758"
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ISWDVSFVTLNFLVPGLVIVISYSKILQIRVSQQDFRLFRTLFLLMVSFFIMWSPIII
TILLILIQNFKQDLVIWPSLFFWVVAFTFANSALNPILYNMTLRVFRHRVLEIRDKLW
PLTILHKFSSGTSLPLGHTHTQAHTHTHAHTHLHT"
ORIGIN

Query Match 24.4%; Score 425; DB 6; Length 933;
Best Local Similarity 100.0%; Pred. No. 3.4e-235;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        149 CGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTG 208
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Db          1 CGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTG 60

Qy        209 CTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCC 268
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Db         61 CTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCC 120

Qy        269 TGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTG 328
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Db        121 TGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTG 180

Qy        329 CTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTC 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTC 240

Qy        389 TACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAG 448
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Db        241 TACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAG 300

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Db        301 CGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGG 360

Qy        509 GCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTC 568
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Qy        569 TTCTT 573
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Db        421 TTCTT 425
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RESULT 13
AX549396
LOCUS AX549396 1737 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 681 from Patent WO02061087.
ACCESSION AX549396
VERSION AX549396.1 GI:25814008
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 681 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1737
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 22.4%; Score 391; DB 6; Length 1737;
Best Local Similarity 99.3%; Pred. No. 2.3e-215;
Matches 711; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy        651 GAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCA 710
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Db        651 GAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCA 710

Qy        711 TTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGG 770
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Db        711 TTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACCG 770
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Qy        771 TAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCT 830
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Db        771 TAAGCCTGGCCTACTCGGAGACCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCT 830

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Db        831 TCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCA 890

Qy        891 CCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCT 950
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Db        891 CCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCT 950

Qy        951 TCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACA 1010
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Db        951 TCTTCTGGGTGGTCCCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACA 1010

Qy       1011 TGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGG 1070
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Db       1011 TGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGG 1070

Qy       1071 GAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAAT 1130
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Db       1071 GAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAA- 1129

Qy       1131 TTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTT 1190
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Db       1130 TTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTT 1189

Qy       1191 CATTTCCAGTACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGA 1250
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RESULT 14
AX230123
LOCUS AX230123 1104 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 10 from Patent WO0162797.
ACCESSION AX230123
VERSION AX230123.1 GI:15592145
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Vogeli,G., Wood,L.S., Parodi,L.A. and Lind,P.
TITLE Novel g protein-coupled receptors
JOURNAL Patent: WO 0162797-A 10 30-AUG-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES Location/Qualifiers
source 1. .1104
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ORIGIN

Query Match 18.7%; Score 326; DB 6; Length 1104;
Best Local Similarity 100.0%; Pred. No. 1.7e-177;
Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         27 CGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTC 86

Qy        308 ATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCC 367
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Db         87 ATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCC 146

Qy        368 GTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACG 427
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Db        147 GTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACG 206

Qy        428 CTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGG 487
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Qy        488 GGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTC 547
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Db        327 GCCGCTCTGCCTCTCTGCGTCTTCTT 352
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RESULT 15
BD212934
LOCUS BD212934 300 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel human genes and gene expression products ii.
ACCESSION BD212934
VERSION BD212934.1 GI:33022704
KEYWORDS JP 2002519000-A/1076.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 300)
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.S.,
Reinhard,C., Giese,K., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V., Jones,L.W.
and Crain,B.S.
TITLE Novel human genes and gene expression products ii
JOURNAL Patent: JP 2002519000-A 1076 02-JUL-2002;
CHIRON CORP,HYSEQ INC
COMMENT OS Homo sapiens (human)
PN JP 2002519000-A/1076
PD 02-JUL-2002
PF 28-JAN-1999 JP 2000556580
PR 28-JAN-1998 US 60/072910,24-FEB-1998 US 60/075954 PR
31-MAR-1998 US 60/080114,03-APR-1998 US 60/080515 PR
03-APR-1998 US 60/080666,21-OCT-1998 US 60/105234 PR
28-OCT-1998 US 60/105877
PI LOUIS T WILLIAMS,JAIME ESCOBEDO,MICHAEL A INNIS,PABLO PI
DOMINGUEZ GARCIA,
PI JULIE SUDDUTH KLINGER,CHRISTOPH REINHARD,KLAUSE GIESE,FILIPPO
PI RANDAZZO,
PI GIULIA C KENNEDY,DAVID POT,ALTAF KASSAM,GEORGE LAMSON,RADOJE
PI DRMANAC,
PI RADOMIR CRKVENJAKOV,MARK DICKSON,SNEZANA DRMANAC,IVAN LABAT,
PI DENA LESHKOWITZ,DAVID KITA,VERONICA GARCIA,LEE WILLIAM JONES,
PI BIRJIT STACHE CRAIN
PC C12N15/09,C12N15/09,C07K14/47,C07K14/82,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
Novel human genes and gene expression products ii FH Key
Location/Qualifiers
FT source 1. .300
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 17.2%; Score 300; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.1e-162;

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Db          1 TGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAA 60

Qy       1036 GAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGT 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGT 120

Qy       1096 CAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCAC 1155
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Qy       1156 ACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTGC 1215
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Qy       1216 ACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAGG 1275
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Search completed: October  1, 2004, 01:41:55
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 19:01:32 ; Search time 635.881 Seconds
(without alignments)
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Title: US-10-077-698-2
Perfect score: 1743
Sequence: 1 tccggactagttctagaccg.....aaaaaaaaaaaaaagggcgg 1743

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1743	100.0	1743	3	AAA64346	Aaa64346 DNA encod
2	1743	100.0	1743	6	ABQ81226	Abq81226 Human 142
3	1328	76.2	1458	4	AAI66039	Aai66039 Human G p
4	1109	63.6	1160	7	ABX10627	Abx10627 DNA encod
5	1086	62.3	1086	6	ABS73343	Abs73343 cDNA enco
6	1081	62.0	1321	4	AAD08854	Aad08854 Human G-p
7	1035	59.4	1086	6	ABS73398	Abs73398 DNA encod
8	1035	59.4	1086	7	ACA60998	Aca60998 cDNA enco
9	1035	59.4	1086	8	ADB47641	Adb47641 Human cDN
10	984	56.5	1086	6	ABS73399	Abs73399 DNA encod
11	926	53.1	1086	6	ABT04869	Abt04869 Human G p
12	913	52.4	1742	3	AAZ49745	Aaz49745 Human 142
13	746	42.8	746	5	ABA21432	Aba21432 Human ner
14	586	33.6	632	7	ACA61000	Aca61000 Novel hum
15	586	33.6	632	8	ADB47644	Adb47644 Human cDN
16	559	32.1	1066	9	ADC87012	Adc87012 Human GPC
17	550	31.6	3173	4	AAC82670	Aac82670 Human 7TM
18	425	24.4	933	9	ADC12755	Adc12755 Human GPC
19	391	22.4	1737	7	ABZ42599	Abz42599 Human G p
20	337	19.3	388	4	ABA08489	Aba08489 Human GPC
21	326	18.7	1104	4	AAS42815	Aas42815 Human G P
22	300	17.2	300	2	AAZ13607	Aaz13607 Human gen
23	298	17.1	760	2	AAX99045	Aax99045 Human val
24	198	11.4	300	2	AAX98319	Aax98319 Human can
25	143	8.2	300	2	AAX98320	Aax98320 Human can
26	131	7.5	638	6	AAS62901	Aas62901 Human G p
27	111	6.4	426	4	AAS42838	Aas42838 Human G P
28	67	3.8	3955	4	AAK66108	Aak66108 Human imm
29	67	3.8	11684	4	AAK66109	Aak66109 Human imm
30	67	3.8	12458	4	AAK66107	Aak66107 Human imm
31	66	3.8	700	4	AAH92222	Aah92222 Human inf
c 32	66	3.8	25871	3	AAA09888	Aaa09888 Human gen
c 33	65	3.7	178896	6	ABQ88146	Abq88146 Human ost
c 34	58	3.3	162450	3	AAZ86967	Aaz86967 Retinobla
c 35	57	3.3	80	7	ACA61001	Aca61001 Novel hum
c 36	57	3.3	80	8	ADB47645	Adb47645 Human GPC
c 37	57	3.3	19553	4	ABK42538	Abk42538 Genomic s
c 38	57	3.3	19553	8	ADB60694	Adb60694 Connectiv
c 39	55	3.2	319	7	ABZ71836	Abz71836 Human can
40	55	3.2	598	4	AAK66647	Aak66647 Human imm
c 41	55	3.2	14970	4	AAS42037	Aas42037 Genomic s
c 42	55	3.2	14976	4	AAS42038	Aas42038 Genomic s
c 43	55	3.2	27827	8	ADA02810	Ada02810 Human Fis
c 44	55	3.2	27827	9	ADB72548	Adb72548 Human CA
c 45	55	3.2	27828	9	ADC85290	Adc85290 Human gen

ALIGNMENTS

RESULT 1
AAA64346
ID AAA64346 standard; DNA; 1743 BP.
XX
AC AAA64346;
XX
DT 20-DEC-2000 (first entry)
XX
DE DNA encoding a human G-protein coupled receptor designated 14273.
XX
KW Human; G-protein coupled receptor; receptor-mediated disorder;
KW 14273 receptor; cardiovascular disease; congestive heart failure;
KW cardiac myocyte hypertrophy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 44. .1129
FT /*tag= a
FT /product= "G-protein coupled receptor 14273"
XX
PN WO200050596-A2.
XX
PD 31-AUG-2000.
XX
PF 28-FEB-2000; 2000WO-US005068.
XX
PR 26-FEB-1999; 99US-00261599.
PR 08-DEC-1999; 99US-00456455.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Glucksmann MA, Tsai F;
XX
DR WPI; 2000-587184/55.
DR P-PSDB; AAB08538.
XX
PT 14273 receptor polynucleotides and polypeptides, useful in the diagnosis
PT and treatment of receptor-mediated disorders such as cardiovascular
PT diseases.
XX
PS Claim 3; Fig 1; 105pp; English.
XX
CC The present sequence encodes a human G-protein coupled receptor,
CC designated 14273 receptor. The G-protein coupled receptor 14273
CC polypeptide is used to produce antibodies, in drug screening assays, and

```
CC   to screen for agonist and antagonists. The antibodies are used for
CC   diagnostic applications, and to assess abnormal tissue distributions or
CC   abnormal expression during development. The antibodies are also useful
CC   for tissue typing, and in forensic identification, as well as for
CC   inhibiting receptor function. The 14273 polynucleotides can be used to
CC   express the protein, to detect 14273 mRNA, to detect genetic alterations
CC   in the 14273 gene, and as a source of primers and probes. The 14273
CC   polynucleotides and polypeptides are also useful as a target for
CC   diagnosis and treatment of receptor-mediated disorders, especially
CC   cardiovascular diseases such as congestive heart failure caused by
CC   cardiac myocyte hypertrophy
XX
SQ   Sequence 1743 BP; 380 A; 479 C; 451 G; 433 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1743;  DB 3;  Length 1743;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1743;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60
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Db          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60

Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
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Db         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120

Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180

Qy        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240
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Db        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240

Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
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Db        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300

Qy        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360

Qy        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420

Qy        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480
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Db        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480

Qy        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
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Db        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540

Qy        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600

Qy        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660

Qy        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720

Qy        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780

Qy        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840

Qy        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900
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Db        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
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Qy        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
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Db       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080

Qy       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
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Qy       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380

Qy       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440

Qy       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500

Qy       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560

Qy       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620
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Db       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620

Qy       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680
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Db       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680

Qy       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740

Qy       1741 CGG 1743
              |||
Db       1741 CGG 1743


RESULT 2
ABQ81226
ID   ABQ81226 standard; cDNA; 1743 BP.
XX
AC   ABQ81226;
XX
DT   05-DEC-2002  (first entry)
```

XX
DE Human 14273 nucleic acid, associated with metabolic disorder.
XX
KW Human; 14273; metabolic disorder; obesity; diabetes; anorexia; cachexia;
KW anorectic; antidiabetic; anabolic; transgenic animal; gene therapy; gene;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 44. .1129
FT /*tag= a
FT /product= "14273"
XX
PN WO200267868-A2.
XX
PD 06-SEP-2002.
XX
PF 26-FEB-2002; 2002WO-US006131.
XX
PR 26-FEB-2001; 2001US-0271655P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gimeno R, Tsai F;
XX
DR WPI; 2002-698629/75.
DR P-PSDB; ABB79906.
XX
PT Identifying a nucleic acid associated with a metabolic disorder, useful
PT for diagnosing metabolic disorders, e.g. obesity, comprises contacting
PT the sample with a probe comprising at least 25 contiguous nucleotides of
PT the 14273 gene.
XX
PS Claim 1; Fig 1A-B; 95pp; English.
XX
CC The present sequence is that of a human nucleic acid, designated 14273,
CC associated with metabolic disorders. 14273 molecules are expressed at
CC high levels in adipose tissue, e.g. white adipose tissue and brown
CC adipose tissue, as well as in pancreatic islets. They are upregulated
CC during exposure to cold (i.e. under conditions that affect brown or white
CC adipocyte metabolism) and downregulated in genetic models of obesity.
CC 14273 knock-out mice, when fed a high-fat diet, gain more weight and have
CC larger epididymal fat pads than wild-type mice. They also show increased
CC levels of glucose and insulin upon fasting. A 14273 agonist may be
CC beneficial to the treatment of obesity and/or type II diabetes by
CC preventing fat accumulation on a high-fat diet and/or the increases in
CC endogenous glucose production which occur in type II diabetes. The
CC present invention provides 14273 nucleic acids, polypeptides and
CC antibodies useful for the diagnosis and treatment of metabolic disorders
CC including obesity, anorexia, cachexia and diabetes. Also provided are
CC methods for identifying a subject having a metabolic disorder, for
CC identifying a compound capable of modulating metabolic activity, methods
CC for modulating metabolic activity or adipocyte activity (hyperplastic
CC growth, hypertrophic growth or lipogenesis), methods for modulating
CC lipogenesis or lipolysis in a subject, and a method for regulating
CC endogenous glucose levels
XX
SQ Sequence 1743 BP; 380 A; 479 C; 451 G; 433 T; 0 U; 0 Other;

Query Match 100.0%; Score 1743; DB 6; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60
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Db          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60

Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120

Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180

Qy        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240
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Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
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Db        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300

Qy        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
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Db        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360

Qy        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420

Qy        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480
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Qy        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
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Db        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540

Qy        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600

Qy        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660
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Db        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660

Qy        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720

Qy        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780

Qy        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840

Qy        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
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Db        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960

Qy        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
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Db        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020

Qy       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080

Qy       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140

Qy       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
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Qy       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
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Db       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260

Qy       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380

Qy       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1441 TACTAAAAATAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
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Db       1441 TACTAAAAATAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500

Qy       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560
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Db       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560

Qy       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620
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Db       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620

Qy       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680

Qy       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAAGGG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAAGGG 1740

Qy       1741 CGG 1743
             |||
Db       1741 CGG 1743
```

```
RESULT 3
AAI66039
ID   AAI66039 standard; cDNA; 1458 BP.
XX
AC   AAI66039;
XX
DT   08-JAN-2002  (first entry)
XX
DE   Human G protein-coupled receptor encoding cDNA SEQ ID NO 2.
XX
KW   Human; G protein-coupled receptor; cytostatic; cancer; hypohypophysism;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             58. .1143
FT                   /*tag=  a
FT                   /product= "G protein-coupled receptor"
FT                   /note= "claimed in claim 6"
XX
PN   JP2001211885-A.
XX
PD   07-AUG-2001.
XX
PF   02-FEB-2000; 2000JP-00024921.
XX
PR   02-FEB-2000; 2000JP-00024921.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
DR   WPI; 2001-629567/73.
DR   P-PSDB; AAM51426.
XX
PT   A new G protein-coupled receptor polypeptide.
XX
PS   Claim 6; Page 41-42; 52pp; Japanese.
XX
CC   The invention relates to a human G protein-coupled receptor polypeptide
CC   with cytostatic activity and used for the treatment of cancers or
CC   hypohypophysism
XX
SQ   Sequence 1458 BP; 271 A; 445 C; 386 G; 356 T; 0 U; 0 Other;
```

```
  Query Match             76.2%;  Score 1328;  DB 4;  Length 1458;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1428;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 AGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCG 88

Qy         75 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 ACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACG 148

Qy        135 TCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCT 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCT 208

Qy        195 TTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCC 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 TTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCC 268

Qy        255 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 GCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCG 328

Qy        315 CTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCT 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 CTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCT 388

Qy        375 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCG 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 GCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCG 448

Qy        435 CGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTG 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 CGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTG 508

Qy        495 GGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTC 554
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        509 GGCGGCGGGCGCGGGCAGTGCTACTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTC 568

Qy        555 TGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAA 614
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        569 TGCCTCTCTGCGTCTTCTTCCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAA 628

Qy        615 TTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTT 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 TTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTT 688

Qy        675 TTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTT 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 TTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTT 748

Qy        735 TACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCC 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 TACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCC 808

Qy        795 ACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGG 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        809 ACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGG 868

Qy        855 TCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGA 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 TCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGA 928
```

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Qy        915 ACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACAT 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 ACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACAT 988

Qy        975 TTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 TTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGA 1048

Qy       1035 AGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTG 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 AGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTG 1108

Qy       1095 TCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCA 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 TCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCA 1168

Qy       1155 CACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTG 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1169 CACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTG 1228

Qy       1215 CACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAG 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 CACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAG 1288

Qy       1275 GGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCA 1334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 GGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCA 1348

Qy       1335 GTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGT 1394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 GTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGT 1408

Qy       1395 CAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTCTACT 1444
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 CAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTCTACT 1458
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RESULT 4
ABX10627
ID ABX10627 standard; DNA; 1160 BP.
XX
AC ABX10627;
XX
DT 11-APR-2003 (first entry)
XX
DE DNA encoding human orphan SNORF49 receptor.
XX
KW Human; gene; ds; SNORF49 receptor; neuroregulator; inflammation;
KW arthritis; autoimmune disease; transplant rejection; infection;
KW septicaemia; AIDS; neurological disorder; schizophrenia; epilepsy;
KW respiratory disorder; asthma; obesity; diabetes; anorexia;
KW cardiovascular disorder; ischaemia; stroke; cancer; sexual disorder;
KW reproductive disorder; circadian rhythm disorder; renal disorder;
KW bone disease; osteoporosis; allergy; Parkinson's disease;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   28. .1113
FT   /*tag= a
FT   /product= "SNORF49 receptor"
XX
PN US2002151705-A1.
XX
PD 17-OCT-2002.
XX
PF 11-DEC-2001; 2001US-00015498.
XX
PR 05-OCT-1999; 99US-00412933.
XX
PA (SMIT/) SMITH K E.
PA (QUAN/) QUAN Y.
XX
PI Smith KE, Quan Y;
XX
DR WPI; 2003-198336/19.
DR P-PSDB; ABG73199.
XX
PT New recombinant nucleic acid comprising a nucleic acid encoding a
PT mammalian SNORF49 receptor, useful for screening antagonist to the
PT SNORF49 receptor or as probes to obtain homologous nucleic acids from
PT other species.
XX
PS Claim 2; Fig 1; 13pp; English.
XX
CC The invention discloses a recombinant nucleic acid comprising a nucleic
CC acid encoding a mammalian SNORF49 receptor, having a sequence identical
CC to the sequence of the human SNORF49 receptor-encoding nucleic acid
CC contained in plasmid pEXJ.T73BS-hS-NORF49-f. SNORF49 receptor is a
CC neuroregulator. The nucleic acid is useful for expressing the receptor in
CC transfected cells, for screening for antagonists to the SNORF49 receptor
CC or as probes to obtain homologous nucleic acids from other species and to
CC detect the existence of nucleic acids having complementary sequences in
CC samples. The receptor can also be used in the design of drugs for
CC treating various pathophysiological conditions, such as inflammation,
CC arthritis, autoimmune disease, transplant rejection, infections,
CC septicaemia, AIDS, neurological disorders, such as schizophrenia and
CC epilepsy, respiratory disorders, asthma, obesity, diabetes, anorexia,
CC cardiovascular disorders, ischaemia, stroke, cancer, sexual/reproductive
CC disorders, circadian rhythm disorders, renal disorders, bone diseases,
CC osteoporosis, allergy, Parkinson's disease and Alzheimer's disease. The
CC sequence presented is the DNA encoding the human orphan SNORF49 receptor
XX
SQ Sequence 1160 BP; 192 A; 372 C; 318 G; 278 T; 0 U; 0 Other;

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  Query Match             63.6%;  Score 1109;  DB 7;  Length 1160;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1159;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 ACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCGAC 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCGAC 60

Qy         77 GCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACGTC 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACGTC 120

Qy        137 AAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTT 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTT 180

Qy        197 GCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGC 240

Qy        257 GGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCT 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCT 300

Qy        317 ATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGC 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGC 360

Qy        377 CACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCG 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCG 420

Qy        437 GTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGG 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGG 480

Qy        497 CGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTG 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTG 540
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Qy        557 CCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAATT 616
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTCTCTGCGTCTTCTTCCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAATT 600

Qy        617 TCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTT 676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTT 660

Qy        677 GTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTA 736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTA 720

Qy        737 CAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCCAC 796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCCAC 780

Qy        797 CAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGTC 856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGTC 840

Qy        857 TCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAAC 916
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAAC 900

Qy        917 TTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATTT 976
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATTT 960

Qy        977 GCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAAG 1036
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAAG 1020

Qy       1037 AAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGTC 1096
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGTC 1080

Qy       1097 AAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCACA 1156
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCACA 1140

Qy       1157 CCTGGCGAGCTGTGGCATGC 1176
              ||||||||||||||||||||
Db       1141 CCTGGCGAGCTGTGGCATGC 1160
```

RESULT 5
ABS73343
ID ABS73343 standard; cDNA; 1086 BP.
XX
AC ABS73343;
XX
DT 04-DEC-2002 (first entry)
XX
DE cDNA encoding human GPCR HF1948.
XX
KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
KW psychotic disorder; asthma; bronchospasm; anaesthesia;
KW myocardial infarction; MI; stroke; glaucoma; anxiety;
KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
KW prostatic hypertrophy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200268600-A2.
XX
PD 06-SEP-2002.
XX
PF 26-FEB-2002; 2002WO-US005625.
XX
PR 26-FEB-2001; 2001US-0271913P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;
PI Lin I, Ortuno D;
XX
DR WPI; 2002-706980/76.
DR P-PSDB; ABG95157.
XX
PT New human G-protein coupled receptor (GPCR), useful for screening agonist
PT or inverse agonist compounds for treating diseases associated with GPCR.
XX
PS Claim 23; Page 122-123; 201pp; English.
XX
CC The present invention relates to transmembrane receptors, particularly
CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-
CC endogenous) versions of the GPCRs, and the polynucleotide sequences
CC encoding them. The GPCRs are useful for screening agonist or inverse
CC agonist compounds for treating diseases associated with GPCR. Diseases
CC that can be treated with such compounds include allergies, hypertension,
CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present
CC sequence encodes an endogenous human GPCR
XX
SQ Sequence 1086 BP; 182 A; 348 C; 295 G; 261 T; 0 U; 0 Other;

Query Match 62.3%; Score 1086; DB 6; Length 1086;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
              ||||||
Db       1081 GGCTAA 1086
```

RESULT 6
AAD08854
ID AAD08854 standard; cDNA; 1321 BP.
XX
AC AAD08854;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human G-protein coupled receptor-20 (GCREC-20) cDNA.
XX
KW Human; G-protein coupled receptor-20; GCREC-20; gene therapy; cirrhosis;
KW transgenic animal; proliferative disorder; actinic keratosis;
KW hepatitis nephrotropic; cancer; breast; bladder; bone marrow; brain;
KW uterus; leukaemia; adenocarcinoma; lymphoma; melanoma; myeloma; epilepsy;
KW stroke; neurological disorder; Alzheimer's disease; Parkinson's disease;
KW nausea; Huntington's disease; multiple sclerosis; dementia;
KW angina pectoris; central nervous system disorder;
KW cardiovascular disorder; hypertension; atherosclerosis;
KW congestive heart failure; gastrointestinal disorder; dysphagia;
KW peptic oesophagitis; spasm; gastritis; anorexia; pyrosis; pancreatitis;
KW Crohn's disease; diarrhoea; autoimmune disorder; anaemia;
KW inflammatory disorder; Acquired Immune Deficiency Syndrome; AIDS;
KW Addison's diseases; allergy; asthma; diabetes mellitus; antithyroid;
KW atopic dermatitis; glomerulonephritis; Grave's disease; psoriasis;
KW rheumatoid arthritis; ulcerative colitis; osteoporosis; antifungal;
KW metabolic disorder; obesity; nootropic; protozoacide; virucide; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 30. .1115
FT /*tag= a
FT /product= "Human GCREC-20 protein"
XX
PN WO200142288-A2.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-US033382.
XX
PR 10-DEC-1999; 99US-0172852P.
PR 22-DEC-1999; 99US-0171732P.
PR 14-JAN-2000; 2000US-0176148P.
PR 21-JAN-2000; 2000US-0177331P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Burford N, Baughn MR, Au-Young J, Yang J, Lu DAM, Reddy R;
XX
DR WPI; 2001-381635/40.
DR P-PSDB; AAE04564.
XX
PT New human G-protein coupled receptor polypeptides for diagnosing,
PT preventing, and treating cell proliferative, neurological,
PT cardiovascular, gastrointestinal, autoimmune and metabolic disorders.
XX
PS Claim 5; Page 167; 175pp; English.
XX
CC The present sequence is human G-protein coupled receptor-20 (GCREC-20)
CC cDNA. GCREC is useful in somatic or germline gene therapy to correct a
CC genetic deficiency, to express a conditionally lethal gene product and to
CC express a protein which affords protection against intracellular
CC parasites and also for diagnosis of disorders associated with expression
CC of GCREC. GCREC is also useful for generating hybridisation probes useful
CC in mapping the naturally occurring genomic sequences and to create
CC knockin humanised animals (pigs) or transgenic animals (mice or rats) to
CC model human diseases. GCREC is used to diagnose, prevent and treat
CC proliferative disorders (actinic keratosis, arteriosclerosis, cirrhosis,
CC hepatitis and cancer); cancer (breast, bladder, bone marrow, brain,
CC uterus cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma)
CC neurological disorders (epilepsy, stroke, Alzheimer's, Huntington's,
CC Parkinson's disease, multiple sclerosis; dementia and other central
CC nervous system disorders); cardiovascular disorders (angina pectoris,
CC hypertension, atherosclerosis, congestive heart failure);
CC gastrointestinal disorders (dysphagia, peptic oesophagitis, oesophageal
CC spasm, gastritis, gastric carcinoma, anorexia, nausea, abdominal angina,
CC pyrosis, pancreatitis, Crohn's disease, diarrhoea); autoimmune/
CC inflammatory disorders (acquired immunodeficiency syndrome (AIDS),
CC Addison's diseases, allergies, anaemia, asthma, diabetes mellitus, atopic
CC dermatitis, glomerulonephritis, Grave's disease, osteoarthritis,
CC psoriasis, rheumatoid arthritis, ulcerative colitis, bacterial, fungal,
CC parasitic, protozoal and helminthic infections) and metabolic disorders
CC (obesity, osteoporosis, viral infections)
XX
SQ Sequence 1321 BP; 243 A; 404 C; 348 G; 326 T; 0 U; 0 Other;

Query Match 62.0%; Score 1081; DB 4; Length 1321;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         32 CAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGC 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 CAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGC 77

Qy         92 CTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGG 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 CTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGG 137

Qy        152 CTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTG 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 CTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTG 197

Qy        212 GGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 GGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGC 257

Qy        272 CTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTG 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTG 317

Qy        332 GCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTAC 391
```

```
Db        318 GCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTAC 377

Qy        392 GTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGC 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGC 437

Qy        452 ATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCA 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCA 497

Qy        512 GTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTC 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTC 557

Qy        572 TTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTG 631
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 TTCCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTG 617

Qy        632 ATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTC 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 ATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTC 677

Qy        692 TTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCA 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 TTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCA 737

Qy        752 TCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCC 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 TCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCC 797

Qy        812 CAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATG 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 CAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATG 857

Qy        872 TGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 TGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTG 917

Qy        932 GTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTA 991
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 GTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTA 977

Qy        992 AACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGC 1051
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 AACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGC 1037

Qy       1052 TTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTG 1111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 TTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTG 1097

Qy       1112 TCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGG 1171
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1098 TCGATTATTTCTGGCTAATTTTTCTTTATAGCAGAGTTTCTCACACCTGGCGAGCTGTGG 1157

Qy       1172 CATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTG 1214
              |||||||||||||||||||||||||||||||||||||||||||
Db       1158 CATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTG 1200
```

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RESULT 7
ABS73398
ID   ABS73398 standard; DNA; 1086 BP.
XX
AC   ABS73398;
XX
DT   04-DEC-2002  (first entry)
XX
DE   DNA encoding human GPCR HF1948 mutant I128F.
XX
KW   Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
KW   hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
KW   psychotic disorder; asthma; bronchospasm; anaesthesia;
KW   myocardial infarction; MI; stroke; glaucoma; anxiety;
KW   prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
KW   prostatic hypertrophy; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200268600-A2.
XX
PD   06-SEP-2002.
XX
PF   26-FEB-2002; 2002WO-US005625.
XX
PR   26-FEB-2001; 2001US-0271913P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Liaw CW,  Chalmers DT,  Behan DP,  Maciejewski-Lenior D,  Leonard JN;
PI   Lin I,  Ortuno D;
XX
DR   WPI; 2002-706980/76.
DR   P-PSDB; ABG95169.
XX
PT   New human G-protein coupled receptor (GPCR), useful for screening agonist
PT   or inverse agonist compounds for treating diseases associated with GPCR.
XX
PS   Example 2; Page 180-181; 201pp; English.
XX
CC   The present invention relates to transmembrane receptors, particularly
CC   endogenous human G-protein coupled receptors (GPCRs), mutant (non-
CC   endogenous) versions of the GPCRs, and the polynucleotide sequences
CC   encoding them. The GPCRs are useful for screening agonist or inverse
CC   agonist compounds for treating diseases associated with GPCR. Diseases
CC   that can be treated with such compounds include allergies, hypertension,
CC   reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
CC   disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),
CC   stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
CC   anxiety, prostatic hypertrophy, rhinitis, and angina. The present
CC   sequence encodes a mutant human GPCR
XX
SQ   Sequence 1086 BP; 181 A; 348 C; 295 G; 262 T; 0 U; 0 Other;

  Query Match             59.4%;  Score 1035;  DB 6;  Length 1086;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420
```

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Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
              ||||||
Db       1081 GGCTAA 1086
```

RESULT 8
ACA60998
ID ACA60998 standard; cDNA; 1086 BP.
XX
AC ACA60998;
XX
DT 04-JUL-2003 (first entry)
XX
DE cDNA encoding novel human G protein coupled receptor HGPRBMY18.
XX
KW Human; G protein coupled receptor; GPCR; HGPRBMY18; cytostatic;
KW nootropic; neuroprotective; antiparkinsonian; antidiabetic;
KW antidepressant; hypotensive; tranquilizer; nephrotropic;
KW cell growth disorder; neurological condition; pituitary gland disorder;
KW colon disorder; breast disorder; lung disorder; prostate disorder;
KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
KW colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
KW sleeplessness; hypertension; anxiety; stress; renal failure; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1083
FT   /*tag= a
FT   /product= "HGPRBMY18"
FT   /note= "Human G protein coupled receptor"
XX
PN US2003022186-A1.
XX
PD 30-JAN-2003.
XX
PF 14-NOV-2001; 2001US-00992331.
XX
PR 14-NOV-2000; 2000US-0248483P.
PR 16-JAN-2001; 2001US-0261782P.
PR 27-JUL-2001; 2001US-0308540P.
XX
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
XX
PI Feder JN, Mintier G, Ramanathan CS;
XX
DR WPI; 2003-416985/39.
DR P-PSDB; ABU09715.
XX
PT New isolated human GPCR, HGPRBMYB18, polynucleotide and polypeptide,
PT useful for treating, diagnosing and preventing disorders such as cancer,
PT neurological conditions, and diseases of the pituitary gland, colon,
PT breast and lungs.
XX
PS Claim 1; Fig 1; 66pp; English.
XX
CC The invention describes a new isolated polynucleotide encoding a human G-
CC protein coupled receptor (GPCR) or its functional fragment. The methods
CC and compositions of the present invention are useful for treating,
CC diagnosing, preventing and screening disorders associated with aberrant
CC cell growth, neurological conditions, and diseases related to the
CC pituitary gland, colon, breast, lungs and prostate. These disorders
CC include Alzheimer's, Parkinson, diabetes, dwarfism, colour blindness,
CC retinal pigmentosa, asthma, depression, schizophrenia, sleeplessness,
CC hypertension, anxiety, stress and renal failure. This sequence encodes
CC novel human G protein coupled receptor HGPRBMY18
XX
SQ Sequence 1086 BP; 182 A; 349 C; 295 G; 260 T; 0 U; 0 Other;

  Query Match   59.4%; Score 1035; DB 7; Length 1086;
  Best Local Similarity 99.9%; Pred. No. 0;
  Matches 1085; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTCCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
              ||||||
Db       1081 GGCTAA 1086


RESULT 9
ADB47641
ID   ADB47641 standard; cDNA; 1086 BP.
XX
AC   ADB47641;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human cDNA encoding GPCR, HGPRBMY18.
XX
KW   Human; ss; gene; G protein-coupled receptor; GPCR; endocrine disorder;
KW   pituitary disorder; growth hormone; prolactin; luteinising hormone;
KW   follicle-stimulating hormone; thyroid-stimulating hormone;
KW   adrenocorticotropin; vasopressin; oxytocin; aberrant growth;
KW   aberrant lactation; aberrant sexual characteristic development;
KW   testosterone; oestrogen; aberrant water homeostasis; hypogonadism;
KW   Addison's disease; hypothyroidism; Cushing's disease; agromegaly;
KW   gigantism; lethargy; osteoporosis; aberrant calcium homeostasis;
KW   aberrant potassium homeostasis; reproductive disorder;
KW   developmental disorder; colon cancer; breast cancer; prostate cancer;
KW   lung cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1086
FT                   /*tag=  b
FT                   /product= "HGPRBMY18"
FT                   /transl_except= (pos:364. .372,aa:Gly-Val)
FT   misc_feature    1. .1083
FT                   /*tag=  a
FT                   /note= "Claimed in claim 1"
FT   misc_feature    4. .1083
FT                   /*tag=  c
FT                   /note= "Claimed in claim 1"
XX
PN   US2003129653-A1.
XX
PD   10-JUL-2003.
XX
PF   30-SEP-2002; 2002US-00262313.
XX
PR   16-JAN-2001; 2001US-0261782P.
PR   27-JUL-2001; 2001US-0308540P.
PR   14-NOV-2001; 2001US-00992331.
XX
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
XX
PI   Feder JN,  Mintier G,  Ramanathan CS,  Hawken DR;
XX
DR   WPI; 2003-678603/64.
DR   P-PSDB; ADB47642.
XX
PT   New human G-protein coupled receptor, HGPRBMY18, useful for treating and
PT   diagnosing disease such as cancer, hypothyroidism, Cushing's disease and
PT   osteoporosis.
XX
PS   Claim 1; Fig 1; 71pp; English.
XX
CC   The invention relate to an isolated human G protein-coupled receptor
CC   (GPCR), HGPRBMY18, polynucleotide encoding a novel human GPCR HGPRBMY18.
CC   Also included are expression vectors, host cells, a fusion protein
CC   comprising HGPRBMY18 and an Fc portion of a human immunoglobulin protein,
CC   an anti-HGPRBMY18 antibody its antigenic epitope, screening a library of
CC   molecules or compounds with a polynucleotide to identify at least one
CC   molecule or compound which specifically binds to the polynucleotide
CC   sequence and screening for candidate compounds capable of modulating
CC   activity of a G-protein coupled receptor-encoding polypeptide. HGPRBMY18
CC   or its (ant)agonist (small molecule, peptide, and antisense molecule) is
CC   useful for treating a disease, disorder, or condition related to the
CC   endocrine, gastrointestinal, reproductive, pulmonary, or neural system.
CC   Diseases include endocrine disorders, disorders of the pituitary,
CC   aberrant growth hormone synthesis and/or secretion, aberrant prolactin
CC   synthesis and/or secretion, aberrant luteinising hormone synthesis and/or
CC   secretion, aberrant follicle-stimulating hormone synthesis and/or
CC   secretion, aberrant thyroid-stimulating hormone synthesis and/or
CC   secretion, aberrant adrenocorticotropin synthesis and/or secretion,
CC   aberrant vasopressin secretion, aberrant oxytocin secretion, aberrant
CC   growth, aberrant lactation, aberrant sexual characteristic development,
CC   aberrant testosterone synthesis and/or secretion, aberrant oestrogen
CC   synthesis and/or secretion, aberrant water homeostasis, hypogonadism,
CC   Addison's disease, hypothyroidism, Cushing's disease, agromegaly,
CC   gigantism, lethargy, osteoporosis, aberrant calcium homeostasis, aberrant
CC   potassium homeostasis, reproductive disorders, developmental disorders,
CC   colon cancer, related proliferative condition of the colon, breast
CC   cancer, related proliferative condition of the breast, prostate cancer,
CC   related proliferative condition of the prostate, lung cancer, and related
CC   proliferative condition of the lung. In addition determining the presence
CC   or amount of expression of HGPRBMY18 is useful for diagnosing a
CC   (susceptibility to a) pathological condition such as colon cancer,
CC   related proliferative condition of the colon, breast cancer, related
CC   proliferative condition of the breast, prostate cancer, related
```

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CC   proliferative condition of the prostate, lung cancer, and related
CC   proliferative condition of the lung. The present sequence encodes
CC   HGPRBMY18.
XX
SQ   Sequence 1086 BP; 182 A; 349 C; 295 G; 260 T; 0 U; 0 Other;

  Query Match             59.4%;  Score 1035;  DB 8;  Length 1086;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
              ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTCCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
              ||||||
Db       1081 GGCTAA 1086


RESULT 10
ABS73399
ID   ABS73399 standard; DNA; 1086 BP.
XX
AC   ABS73399;
XX
DT   04-DEC-2002  (first entry)
XX
DE   DNA encoding human GPCR HF1948 mutant E135N.
XX
KW   Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
KW   hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
KW   psychotic disorder; asthma; bronchospasm; anaesthesia;
KW   myocardial infarction; MI; stroke; glaucoma; anxiety;
KW   prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
KW   prostatic hypertrophy; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200268600-A2.
XX
PD   06-SEP-2002.
XX
PF   26-FEB-2002; 2002WO-US005625.
XX
PR   26-FEB-2001; 2001US-0271913P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Liaw CW,  Chalmers DT,  Behan DP,  Maciejewski-Lenior D,  Leonard JN;
PI   Lin I,  Ortuno D;
XX
DR   WPI; 2002-706980/76.
DR   P-PSDB; ABG95170.
XX
PT   New human G-protein coupled receptor (GPCR), useful for screening agonist
PT   or inverse agonist compounds for treating diseases associated with GPCR.
XX
PS   Example 2; Page 183; 201pp; English.
XX
CC   The present invention relates to transmembrane receptors, particularly
CC   endogenous human G-protein coupled receptors (GPCRs), mutant (non-
CC   endogenous) versions of the GPCRs, and the polynucleotide sequences
CC   encoding them. The GPCRs are useful for screening agonist or inverse
CC   agonist compounds for treating diseases associated with GPCR. Diseases
CC   that can be treated with such compounds include allergies, hypertension,
CC   reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
CC   disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),
CC   stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
CC   anxiety, prostatic hypertrophy, rhinitis, and angina. The present
CC   sequence encodes a mutant human GPCR
XX
SQ   Sequence 1086 BP; 183 A; 348 C; 293 G; 262 T; 0 U; 0 Other;

  Query Match             56.5%;  Score 984;  DB 6;  Length 1086;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1084;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
              ||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGAATCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
              ||||||
Db       1081 GGCTAA 1086
```

RESULT 11
ABT04869
ID ABT04869 standard; cDNA; 1086 BP.
XX
AC ABT04869;
XX
DT 11-OCT-2002 (first entry)
XX
DE Human G protein coupled receptor hRUP31 coding sequence.
XX
KW Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200242461-A2.
XX
PD 30-MAY-2002.
XX
PF 26-NOV-2001; 2001WO-US044386.
XX
PR 27-NOV-2000; 2000US-0253404P.
PR 12-DEC-2000; 2000US-0255366P.
PR 20-FEB-2001; 2001US-0270266P.
PR 20-FEB-2001; 2001US-0270286P.
PR 06-APR-2001; 2001US-0282032P.
PR 06-APR-2001; 2001US-0282356P.
PR 06-APR-2001; 2001US-0282358P.
PR 06-APR-2001; 2001US-0282365P.
PR 14-MAY-2001; 2001US-0290917P.
PR 31-JUL-2001; 2001US-0309208P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX
DR WPI; 2002-566565/60.
DR P-PSDB; ABJ04071.
XX
PT Novel endogenous and non-endogenous versions of G protein-coupled
PT receptor useful for identification of candidate compounds as receptor
PT agonists or antagonists for use as therapeutic agents.
XX
PS Claim 15; Page 61; 84pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC several human G-protein coupled receptors (GPCRs). These can be used in
CC the identification of candidate compounds as receptor agonists or inverse
CC agonists having applicability as therapeutic agents. The present sequence
CC is a GPCR coding sequence of the invention
XX
SQ Sequence 1086 BP; 185 A; 346 C; 295 G; 260 T; 0 U; 0 Other;

Query Match 53.1%; Score 926; DB 6; Length 1086;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1076; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         51 CTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCA 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCA 67

Qy        111 CCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGG 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 CCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGG 127

Qy        171 AGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGG 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGG 187
```

```
Qy        231 TGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCT 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 TGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCT 247

Qy        291 GCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGG 350
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Qy       1071 GAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAA 1129
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RESULT 12
AAZ49745
ID AAZ49745 standard; cDNA; 1742 BP.
XX
AC AAZ49745;
XX
DT 02-MAY-2000 (first entry)
XX
DE Human 14273 G-protein coupled receptor (GPCR) encoding cDNA.
XX
KW G-protein coupled receptor; GPCR; 14273 receptor; human; somatostatin;
KW cellular function/activity; galanin receptor; chemokine receptor;
KW diagnosis; treatment; receptor-mediated disorder; screening; ss.
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OS Homo sapiens.
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FH Key   Location/Qualifiers
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FT   /note= "Homologous to galanin receptor, chemokine
FT   receptor and somatostatin"
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FT   /note= "Encodes Val"
XX
PN WO200000611-A2.
XX
PD 06-JAN-2000.
XX
PF 30-JUN-1999; 99WO-US014842.
XX
PR 30-JUN-1998; 98US-00107761.
PR 30-DEC-1998; 98US-00223538.
PR 26-FEB-1999; 99US-00261599.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA, Tsai F;
XX
DR WPI; 2000-147268/13.
DR P-PSDB; AAY44662.
XX
PT Novel G-protein coupled receptor 14273 polynucleotides and polypeptides
PT used as a target for diagnosis and treatment of receptor-mediated
PT disorders.
XX
PS Claim 3a; Fig 1; 89pp; English.
XX
CC The present sequence is the cDNA encoding human G-protein coupled
CC receptor (GPCR) 14273 protein. It is derived from human foetal brain cDNA
CC library using expressed sequence tag (EST) that has homology to GPCR
CC sequences. It is involved in modulation of a cellular function/activity
CC upon binding of a ligand to the GPCR. The GPCR 14273 protein has homology
CC to galanin receptor, chemokine receptor and somatostatin. GPCR 14273
CC sequences are useful as a target for diagnosis and treatment of receptor
CC mediated disorders. The polypeptide is used for screening of drugs,
CC agonist, antagonists and to produce antibodies. The antibodies are used
CC for diagnosis, to assess abnormal tissue distribution or expression
CC during development, inhibiting receptor function, tissue typing and
CC forensic identification. The DNA sequences are used to detect genetic
CC alterations in the gene and as a source of primers and probes
XX
SQ Sequence 1742 BP; 379 A; 490 C; 439 G; 431 T; 0 U; 3 Other;

  Query Match   52.4%; Score 913; DB 3; Length 1742;
  Best Local Similarity 99.1%; Pred. No. 5.3e-311;
  Matches 1613; Conservative   0; Mismatches   14; Indels   0; Gaps   0;

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Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
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Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
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Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
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Qy        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
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RESULT 13
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DT 23-JAN-2002 (first entry)
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KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001334.
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PR 31-JAN-2000; 2000US-0179065P.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-541565/60.
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
PS Disclosure; SEQ ID NO 13763; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are

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CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC   the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC   ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC   breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC   disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC   multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC   cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC   ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC   infectious diseases such as viral, bacterial, fungal and parasitic
CC   infections. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 746 BP; 224 A; 149 C; 164 G; 209 T; 0 U; 0 Other;

  Query Match             42.8%;  Score 746;  DB 5;  Length 746;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-252;
  Matches  746;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        976 TGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAA 1035
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Db          1 TGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAA 60

Qy       1036 GAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGT 1095
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Db         61 GAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGT 120

Qy       1096 CAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCAC 1155
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Db        121 CAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCAC 180

Qy       1156 ACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTGC 1215
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Db        181 ACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCATCAGTGC 240

Qy       1216 ACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAGG 1275
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Db        241 ACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAGG 300

Qy       1276 GGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCAG 1335
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Db        301 GGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCAG 360

Qy       1336 TGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTC 1395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTC 420

Qy       1396 AGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTCTACTAAAAATAAAAA 1455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTCTACTAAAAATAAAAA 480

Qy       1456 AAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTACTTGGGAGGCTGAAC 1515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTACTTGGGAGGCTGAAC 540

Qy       1516 CAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGC 1575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGC 600

Qy       1576 ACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAAAAAAAAAAAGATTTGT 1635
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Db        601 ACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAAAAAAAAAAAGATTTGT 660

Qy       1636 TATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATATGATCAAATTTAATA 1695
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Db        661 TATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATATGATCAAATTTAATA 720

Qy       1696 AATATTTATTTATGACTGTTCAGCAA 1721
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Db        721 AATATTTATTTATGACTGTTCAGCAA 746
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RESULT 14
ACA61000
ID   ACA61000 standard; DNA; 632 BP.
XX
AC   ACA61000;
XX
DT   04-JUL-2003  (first entry)
XX
DE   Novel human G protein coupled receptor HGPRBMY18 3'UTR.
XX
KW   Human; G protein coupled receptor; GPCR; HGPRBMY18; cytostatic;
KW   nootropic; neuroprotective; antiparkinsonian; antidiabetic;
KW   antidepressant; hypotensive; tranquilizer; nephrotropic;
KW   cell growth disorder; neurological condition; pituitary gland disorder;
KW   colon disorder; breast disorder; lung disorder; prostate disorder;
KW   Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
KW   colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
KW   sleeplessness; hypertension; anxiety; stress; renal failure; 3'UTR;
KW   untranslated region; ds.
XX
OS   Homo sapiens.
XX
PN   US2003022186-A1.
XX
PD   30-JAN-2003.
XX
PF   14-NOV-2001; 2001US-00992331.
XX
PR   14-NOV-2000; 2000US-0248483P.
PR   16-JAN-2001; 2001US-0261782P.
PR   27-JUL-2001; 2001US-0308540P.
XX
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
XX
PI   Feder JN,  Mintier G,  Ramanathan CS;
XX
DR   WPI; 2003-416985/39.
XX
PT   New isolated human GPCR, HGPRBMYB18, polynucleotide and polypeptide,
PT   useful for treating, diagnosing and preventing disorders such as cancer,
PT   neurological conditions, and diseases of the pituitary gland, colon,
PT   breast and lungs.
XX
PS   Disclosure; Fig 4; 66pp; English.
XX
CC   The invention describes a new isolated polynucleotide encoding a human G-
CC   protein coupled receptor (GPCR) or its functional fragment. The methods
CC   and compositions of the present invention are useful for treating,
CC   diagnosing, preventing and screening disorders associated with aberrant
CC   cell growth, neurological conditions, and diseases related to the
CC   pituitary gland, colon, breast, lungs and prostate. These disorders
CC   include Alzheimer's, Parkinson, diabetes, dwarfism, colour blindness,
CC   retinal pigmentosa, asthma, depression, schizophrenia, sleeplessness,
CC   hypertension, anxiety, stress and renal failure. This sequence represents
CC   novel human G protein coupled receptor HGPRBMY18 3' untranslated region
CC   (UTR)
XX
SQ   Sequence 632 BP; 219 A; 113 C; 134 G; 166 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 586;  DB 7;  Length 632;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-196;
  Matches  586;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1130 TTTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGT 1189
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Db          1 TTTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGT 60

Qy       1190 TCATTTCCAGTACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAG 1249
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Db         61 TCATTTCCAGTACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAG 120
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Qy       1250 ACATCCACAGCGTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTA 1309
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Db        121 ACATCCACAGCGTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTA 180

Qy       1310 TAAAAGGATTTGTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGG 1369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAAAAGGATTTGTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGG 240

Qy       1370 CTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAG 1429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAG 300

Qy       1430 ACCCCCGTCTCTACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGT 1489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCCCCGTCTCTACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGT 360

Qy       1490 AATCCTAGCTACTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTT. 1549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATCCTAGCTACTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTT 420

Qy       1550 GCAGTGAGCCGAGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATC 1609
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Db        421 GCAGTGAGCCGAGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATC 480

Qy       1610 TTAAAAAAAAAAAAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTG 1669
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Db        481 TTAAAAAAAAAAAAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTG 540

Qy       1670 TGTTTGTAATATGATCAAATTTAATAAATATTTATTTATGACTGTT 1715
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Db        541 TGTTTGTAATATGATCAAATTTAATAAATATTTATTTATGACTGTT 586
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RESULT 15
ADB47644
ID ADB47644 standard; cDNA; 632 BP.
XX
AC ADB47644;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding GPCR, HGPRBMY18, 3' UTR.
XX
KW Human; ss; gene; G protein-coupled receptor; GPCR; endocrine disorder;
KW pituitary disorder; growth hormone; prolactin; luteinising hormone;
KW follicle-stimulating hormone; thyroid-stimulating hormone;
KW adrenocorticotropin; vasopressin; oxytocin; aberrant growth;
KW aberrant lactation; aberrant sexual characteristic development;
KW testosterone; oestrogen; aberrant water homeostasis; hypogonadism;
KW Addison's disease; hypothyroidism; Cushing's disease; agromegaly;
KW gigantism; lethargy; osteoporosis; aberrant calcium homeostasis;
KW aberrant potassium homeostasis; reproductive disorder;
KW developmental disorder; colon cancer; breast cancer; prostate cancer;
KW lung cancer; untranslated region.
XX
OS Homo sapiens.
XX
PN US2003129653-A1.
XX
PD 10-JUL-2003.
XX
PF 30-SEP-2002; 2002US-00262313.
XX
PR 16-JAN-2001; 2001US-0261782P.
PR 27-JUL-2001; 2001US-0308540P.
PR 14-NOV-2001; 2001US-00992331.
XX
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.
XX
PI Feder JN, Mintier G, Ramanathan CS, Hawken DR;
XX
DR WPI; 2003-678603/64.
XX
PT New human G-protein coupled receptor, HGPRBMY18, useful for treating and
PT diagnosing disease such as cancer, hypothyroidism, Cushing's disease and
PT osteoporosis.
XX
PS Disclosure; Fig 4; 71pp; English.
XX
CC The invention relate to an isolated human G protein-coupled receptor
CC (GPCR), HGPRBMY18, polynucleotide encoding a novel human GPCR HGPRBMY18.
CC Also included are expression vectors, host cells, a fusion protein
CC comprising HGPRBMY18 and an Fc portion of a human immunoglobulin protein,
CC an anti-HGPRBMY18 antibody its antigenic epitope, screening a library of
CC molecules or compounds with a polynucleotide to identify at least one
CC molecule or compound which specifically binds to the polynucleotide
CC sequence and screening for candidate compounds capable of modulating
CC activity of a G-protein coupled receptor-encoding polypeptide. HGPRBMY18
CC or its (ant)agonist (small molecule, peptide, and antisense molecule) is
CC useful for treating a disease, disorder, or condition related to the
CC endocrine, gastrointestinal, reproductive, pulmonary, or neural system.
CC Diseases include endocrine disorders, disorders of the pituitary,
CC aberrant growth hormone synthesis and/or secretion, aberrant prolactin
CC synthesis and/or secretion, aberrant luteinising hormone synthesis and/or
CC secretion, aberrant follicle-stimulating hormone synthesis and/or
CC secretion, aberrant thyroid-stimulating hormone synthesis and/or
CC secretion, aberrant adrenocorticotropin synthesis and/or secretion,
CC aberrant vasopressin secretion, aberrant oxytocin secretion, aberrant
CC growth, aberrant lactation, aberrant sexual characteristic development,
CC aberrant testosterone synthesis and/or secretion, aberrant oestrogen
CC synthesis and/or secretion, aberrant water homeostasis, hypogonadism,
CC Addison's disease, hypothyroidism, Cushing's disease, agromegaly,
CC gigantism, lethargy, osteoporosis, aberrant calcium homeostasis, aberrant
CC potassium homeostasis, reproductive disorders, developmental disorders,
CC colon cancer, related proliferative condition of the colon, breast
CC cancer, related proliferative condition of the breast, prostate cancer,
CC related proliferative condition of the prostate, lung cancer, and related
CC proliferative condition of the lung. In addition determining the presence
CC or amount of expression of HGPRBMY18 is useful for diagnosing a
CC (susceptibility to a) pathological condition such as colon cancer,
CC related proliferative condition of the colon, breast cancer, related
CC proliferative condition of the breast, prostate cancer, related
CC proliferative condition of the prostate, lung cancer, and related
CC proliferative condition of the lung. The present sequence represents the
CC 5' or 3' UTR of the cDNA encoding HGPRBMY18.
XX
SQ Sequence 632 BP; 219 A; 113 C; 134 G; 166 T; 0 U; 0 Other;

Query Match 33.6%; Score 586; DB 8; Length 632;
Best Local Similarity 100.0%; Pred. No. 3.5e-196;
Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1130 TTTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGT 1189
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Db          1 TTTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGT 60

Qy       1190 TCATTTCCAGTACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAG 1249
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Db        121 ACATCCACAGCGTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTA 180

Qy       1310 TAAAAGGATTTGTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGG 1369
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Db        181 TAAAAGGATTTGTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGG 240

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Db        241 CTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAG 300
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Qy       1430 ACCCCCGTCTCTACTAAAAATAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGT 1489
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Qy       1490 AATCCTAGCTACTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTT 1549
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Db        361 AATCCTAGCTACTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTT 420

Qy       1550 GCAGTGAGCCGAGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATC 1609
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Db        421 GCAGTGAGCCGAGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATC 480

Qy       1610 TTAAAAAAAAAAAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTG 1669
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Db        481 TTAAAAAAAAAAAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTG 540

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Job time : 640.881 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 21:45:48 ; Search time 138.258 Seconds
(without alignments)
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Perfect score: 1743
Sequence: 1 tccggactagttctagaccg.....aaaaaaaaaaaaaagggcgg 1743

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Post-processing: Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2		1743	100.0	1743	4	US-09-456-455A-2	Sequence 2, Appli
c 3		58	3.3	162450	4	US-09-345-882-1	Sequence 1, Appli
4		50	2.9	2191	4	US-09-482-273-79	Sequence 79, Appl
c 5		50	2.9	26664	4	US-09-564-805-28	Sequence 28, Appl
6		50	2.9	39982	4	US-09-820-924-3	Sequence 3, Appli
7		49	2.8	2094	4	US-09-369-247-46	Sequence 46, Appl
8		48	2.8	405	4	US-09-621-976-14833	Sequence 14833, A
9		48	2.8	431	4	US-09-621-976-15040	Sequence 15040, A
c 10		48	2.8	44848	4	US-09-435-739-42	Sequence 42, Appl
c 11		47	2.7	128779	4	US-09-497-855A-38	Sequence 38, Appl
c 12		45	2.6	7676	1	US-08-451-777A-7	Sequence 7, Appli
c 13		45	2.6	7676	2	US-08-451-778A-7	Sequence 7, Appli
c 14		45	2.6	7676	2	US-08-998-208-7	Sequence 7, Appli
c 15		45	2.6	7676	5	PCT-US95-06743-7	Sequence 7, Appli
16		45	2.6	38844	4	US-09-734-675-3	Sequence 3, Appli
c 17		45	2.6	118067	4	US-09-497-855A-32	Sequence 32, Appl
18		44	2.5	433	4	US-09-621-976-18603	Sequence 18603, A
19		44	2.5	577	4	US-09-227-357-92	Sequence 92, Appl
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21		44	2.5	1560	4	US-09-456-455A-5	Sequence 5, Appli
c 22		44	2.5	176373	3	US-09-128-155-17	Sequence 17, Appl
23		44	2.5	786431	4	US-09-751-389-3	Sequence 3, Appli
24		42	2.4	955	4	US-09-641-638-19	Sequence 19, Appl
25		42	2.4	955	4	US-09-641-638-20	Sequence 20, Appl
c 26		42	2.4	20674	4	US-09-641-638-651	Sequence 651, App
c 27		42	2.4	28001	4	US-09-819-993-3	Sequence 3, Appli
c 28		42	2.4	28001	4	US-10-193-295-3	Sequence 3, Appli
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c 33		42	2.4	66804	4	US-09-740-041-3	Sequence 3, Appli
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35		41	2.4	90541	4	US-09-759-359A-3	Sequence 3, Appli
c 36		40	2.3	514	4	US-09-621-976-17509	Sequence 17509, A
37		40	2.3	548	4	US-09-495-050A-91	Sequence 91, Appl
38		40	2.3	6792	4	US-09-374-454-20	Sequence 20, Appl
39		40	2.3	11613	1	US-08-484-044-10	Sequence 10, Appl
c 40		40	2.3	35100	1	US-08-306-691B-19	Sequence 19, Appl
c 41		40	2.3	35100	5	PCT-US93-06251-19	Sequence 19, Appl
42		40	2.3	41684	4	US-09-536-059-1	Sequence 1, Appli
c 43		40	2.3	48763	4	US-09-916-204-3	Sequence 3, Appli
c 44		40	2.3	50000	4	US-09-146-053-3	Sequence 3, Appli
c 45		40	2.3	786431	4	US-09-751-389-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-261-599B-2
; Sequence 2, Application US/09261599B
; Patent No. 6395877
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 14273 Receptor, A No. 6395877el G-Protein Coupled Receptor
; FILE REFERENCE: 5800-4B, 035800/177086
; CURRENT APPLICATION NUMBER: US/09/261,599B
; CURRENT FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/107,761
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-261-599B-2

Query Match 100.0%; Score 1743; DB 4; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60

Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120

Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180

Qy        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240
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Db        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240

Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
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Db        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300

Qy        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
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Db        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
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Qy       361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
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Db       361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420

Qy       421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480
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Db       421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480

Qy       481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
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Db       481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540

Qy       541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600
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Db       541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600

Qy       601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660
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Db       601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660

Qy       661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720
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Db       661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720

Qy       721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780

Qy       781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840
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Db       781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840

Qy       841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900
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Db       841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy       901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
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Db       901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960

Qy       961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
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Db       961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020

Qy      1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
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Db      1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080

Qy      1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
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Db      1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140

Qy      1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
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Db      1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200

Qy      1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260

Qy      1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy      1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380

Qy      1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
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Db      1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440

Qy      1441 TACTAAAAATAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
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Qy      1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560
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Qy      1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620
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Qy      1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680
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Db      1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680

Qy      1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740
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Db      1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740

Qy      1741 CGG 1743
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Db      1741 CGG 1743
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RESULT 2
US-09-456-455A-2
; Sequence 2, Application US/09456455A
; Patent No. 6448005
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: 14273 Receptor, A No. 6448005el G-Protein Coupled Receptor
; FILE REFERENCE: MNI-204CP3
; CURRENT APPLICATION NUMBER: US/09/456,455A
; CURRENT FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 09/107,761
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-456-455A-2

Query Match 100.0%; Score 1743; DB 4; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
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Db         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120

Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
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Qy        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240
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Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
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Db        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300

Qy        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
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Db        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360

Qy        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
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Db        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420

Qy        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480
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Qy        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
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Qy        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600
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Qy        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660
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Db        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660

Qy        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720
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Db        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720

Qy        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780
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Db        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780

Qy        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840
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Db        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840

Qy        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900
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Db        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
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Db        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960

Qy        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
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Qy       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
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Qy       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
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Qy       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
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Qy       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
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Qy       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
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Db       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
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Qy       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
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Qy       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
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Qy       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620
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Qy       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680
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Qy       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740
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Db       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740

Qy       1741 CGG 1743
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Db       1741 CGG 1743
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RESULT 3
US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele

; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99117
; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
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; LOCATION: 106940
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; LOCATION: 108106
; OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108149
; OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108308
; OTHER INFORMATION: 5-135-357 : polymorphic base A or G
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; NAME/KEY: allele
; LOCATION: 108471
; OTHER INFORMATION: 5-136-174 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134134
; OTHER INFORMATION: 5-140-120 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134362
; OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134374
; OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
; FEATURE:
; NAME/KEY: allele
; LOCATION: 146328
; OTHER INFORMATION: 5-143-84 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 146345
; OTHER INFORMATION: 5-143-101 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 150329
; OTHER INFORMATION: 5-145-24 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 160031
; OTHER INFORMATION: 5-148-352 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72771..72817
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; NAME/KEY: allele
; LOCATION: 72771..72817
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; NAME/KEY: allele
; LOCATION: 88050..88096
; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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; NAME/KEY: allele
; LOCATION: 88050..88096
; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
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; NAME/KEY: allele
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; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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; LOCATION: 90819..90865
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; LOCATION: 93690..93736
; OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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; NAME/KEY: allele
; LOCATION: 93690..93736
; OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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; LOCATION: 97099..97145
; OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
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; NAME/KEY: allele
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; LOCATION: 97130..97177
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; NAME/KEY: allele
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; OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99075..99121
; OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99094..99140
; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99094..99140
; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59

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;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108127..108177
;   OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108127..108177
;   OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
;   FEATURE:

  Query Match             3.3%;  Score 58;  DB 4;  Length 162450;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-14;
  Matches   58;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1527 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGCACTCCAACC 1584
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8387 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGCACTCCAACC 8330


RESULT 4
US-09-482-273-79
; Sequence 79, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 71 Human Secreted Proteins
;  FILE REFERENCE: PZ030P1
;  CURRENT APPLICATION NUMBER: US/09/482,273
;  CURRENT FILING DATE: 2000-01-13
;  EARLIER APPLICATION NUMBER: PCT/US99/15849
;  EARLIER FILING DATE: 1999-07-14
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/092,922
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/092,956
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 267
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 2191
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1327)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1334)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-482-273-79

  Query Match             2.9%;  Score 50;  DB 4;  Length 2191;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-10;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1361 TTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 1410
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1929 TTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 1978


RESULT 5
US-09-564-805-28/c
; Sequence 28, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
;  APPLICANT:  Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION:  Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE:  2318-258
;  CURRENT APPLICATION NUMBER: US/09/564,805
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/107,468
;  PRIOR FILING DATE:  1998-11-06
;  PRIOR APPLICATION NUMBER:  09/434,382
;  PRIOR FILING DATE:  1999-11-05
;  NUMBER OF SEQ ID NOS:  240
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 26664
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (910)..(13104)
;   OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
;   OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
;   OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
;   OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
;   NAME/KEY: misc_feature
;   LOCATION: (13756)..(22917)
;   OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon
;   OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
;   OTHER INFORMATION: 18583-18701; exon 16: 20349-20445; exon 17:
;   OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
;   NAME/KEY: misc_feature
;   LOCATION: (23045)..(26452)
;   OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon
;   OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23:
;   OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation
;   OTHER INFORMATION: signal: 26447-26452
;   NAME/KEY: variation
;   LOCATION: (826)..(23879)
;   OTHER INFORMATION: s at positions 826 and 23180 is G or C; y at
;   OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
;   OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at
;   OTHER INFORMATION: positions 22211 and 23879 is A or G.
US-09-564-805-28

  Query Match             2.9%;  Score 50;  DB 4;  Length 26664;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-10;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1361 TTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 1410
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17609 TTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 17560


RESULT 6
US-09-820-924-3
; Sequence 3, Application US/09820924
; Patent No. 6555351
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen M. et al
;  TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001213
;  CURRENT APPLICATION NUMBER: US/09/820,924
;  CURRENT FILING DATE:  2001-03-30
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 39982
;   TYPE: DNA
;   ORGANISM: Human
US-09-820-924-3

  Query Match             2.9%;  Score 50;  DB 4;  Length 39982;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-10;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1361 TTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 1410
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22437 TTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 22486


RESULT 7
US-09-369-247-46
; Sequence 46, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 44 Human Secreted Proteins
;  FILE REFERENCE: PZ024P1
;  CURRENT APPLICATION NUMBER: US/09/369,247
;  CURRENT FILING DATE: 1999-08-05
;  EARLIER APPLICATION NUMBER: 60/074,118
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/074,157
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/074,137
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/074,341
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/074,141
;  EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 172
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
;   LENGTH: 2094
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-369-247-46

  Query Match             2.8%;  Score 49;  DB 4;  Length 2094;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-10;
  Matches   49;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1516 CAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGAT 1564
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1975 CAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGAT 2023


RESULT 8
US-09-621-976-14833
; Sequence 14833, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 14833
;   LENGTH: 405
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-14833

  Query Match             2.8%;  Score 48;  DB 4;  Length 405;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-09;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1345 CCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAG 1392
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 CCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAG 238


RESULT 9
US-09-621-976-15040
; Sequence 15040, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15040
;   LENGTH: 431
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15040

  Query Match             2.8%;  Score 48;  DB 4;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-09;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1345 CCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAG 1392
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 CCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGTGGATCACCTGAG 238


RESULT 10
US-09-435-739-42/c
; Sequence 42, Application US/09435739
; Patent No. 6664105
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky, Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY A
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 00/20454
;  CURRENT APPLICATION NUMBER: US/09/435,739
;  CURRENT FILING DATE:  2001-06-05
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
;   LENGTH: 44848
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-435-739-42

  Query Match             2.8%;  Score 48;  DB 4;  Length 44848;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-10;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1361 TTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGAC 1408
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19123 TTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGAC 19076


RESULT 11
US-09-497-855A-38/c
; Sequence 38, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
;  APPLICANT: Huang, Tim
;  TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
;  FILE REFERENCE: UMO1523
;  CURRENT APPLICATION NUMBER: US/09/497,855A
;  CURRENT FILING DATE:  2000-02-04
;  PRIOR APPLICATION NUMBER: 60/120,592
;  PRIOR FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: 60/118,760
;  PRIOR FILING DATE: 1999-02-05
;  NUMBER OF SEQ ID NOS: 54
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;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
;   LENGTH: 128779
;   TYPE: DNA
;   ORGANISM: Homo sapiens;
US-09-497-855A-38

  Query Match             2.7%;  Score 47;  DB 4;  Length 128779;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-09;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1520 AGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCG 1566
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db      94386 AGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCG 94340


RESULT 12
US-08-451-777A-7/c
; Sequence 7, Application US/08451777A
; Patent No. 5789223
;  GENERAL INFORMATION:
;    APPLICANT:  Bergsma, Derk J.
;    APPLICANT:  Stambolian, Dwight
;    TITLE OF INVENTION:  Human Galactokinase Gene
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corp./Corporate
;      ADDRESSEE:  Intellectual Property
;      STREET:  709 Swedeland Road/UW2220
;      CITY:  King of Prussia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/451,777A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10825
;      FILING DATE:  23-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eagle, Alissa M.
;      REGISTRATION NUMBER:  37,126
;      REFERENCE/DOCKET NUMBER:  P50268-1B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5364
;      TELEFAX:  610-270-5090
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7676 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-451-777A-7

  Query Match             2.6%;  Score 45;  DB 1;  Length 7676;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-08;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1527 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 1571
             |||||||||||||||||||||||||||||||||||||||||||||
Db       4083 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 4039


RESULT 13
US-08-451-778A-7/c
; Sequence 7, Application US/08451778A
; Patent No. 5830649
;  GENERAL INFORMATION:
;    APPLICANT:  Bergsma, Derk J.
;    APPLICANT:  Stambolian, Dwight
;    TITLE OF INVENTION:  Human Galactokinase Gene
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corp./Corporate
;      ADDRESSEE:  Intellectual Property
;      STREET:  709 Swedeland Road/UW2220
;      CITY:  King of Prussia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/451,778A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10825
;      FILING DATE:  23-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eagle, Alissa M.
;      REGISTRATION NUMBER:  37,126
;      REFERENCE/DOCKET NUMBER:  P50268-1B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5364
;      TELEFAX:  610-270-5090
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7676 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-451-778A-7

  Query Match             2.6%;  Score 45;  DB 2;  Length 7676;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-08;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1527 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 1571
             |||||||||||||||||||||||||||||||||||||||||||||
Db       4083 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 4039


RESULT 14
US-08-998-208-7/c
; Sequence 7, Application US/08998208
; Patent No. 5880105
;  GENERAL INFORMATION:
;    APPLICANT:  Bergsma, Derk J.
;    APPLICANT:  Stambolian, Dwight
;    TITLE OF INVENTION:  Human Galactokinase Gene
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corp./Corporate
;      ADDRESSEE:  Intellectual Property
;      STREET:  709 Swedeland Road/UW2220
;      CITY:  King of Prussia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,208
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/451,777
;      FILING DATE:  26-MAY-1995
;      APPLICATION NUMBER:  PCT/US94/10825
;      FILING DATE:  23-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eagle, Alissa M.
;      REGISTRATION NUMBER:  37,126
;      REFERENCE/DOCKET NUMBER:  P50268-1B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5364
;      TELEFAX:  610-270-5090
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7676 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-998-208-7

  Query Match             2.6%;  Score 45;  DB 2;  Length 7676;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-08;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1527 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 1571
             |||||||||||||||||||||||||||||||||||||||||||||
Db       4083 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 4039


RESULT 15
PCT-US95-06743-7/c
; Sequence 7, Application PC/TUS9506743
;  GENERAL INFORMATION:
;    APPLICANT:  Bergsma, Derk J.
;    APPLICANT:  Stambolian, Dwight
;    TITLE OF INVENTION:  Human Galactokinase Gene
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corp./Corporate
;      ADDRESSEE:  Intellectual Property
;      STREET:  709 Swedeland Road/UW2220
;      CITY:  King of Prussia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06743
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10825
;      FILING DATE:  23-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sutton, Jeffrey A.
;      REGISTRATION NUMBER:  34,028
;      REFERENCE/DOCKET NUMBER:  P50268-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5024
;      TELEFAX:  610-270-5090
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7676 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US95-06743-7

  Query Match             2.6%;  Score 45;  DB 5;  Length 7676;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-08;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1527 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 1571
             |||||||||||||||||||||||||||||||||||||||||||||
Db       4083 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCA 4039


Search completed: October  1, 2004, 03:56:15
Job time : 141.258 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 21:52:37 ; Search time 817.411 Seconds
(without alignments)
10810.058 Million cell updates/sec

Title: US-10-077-698-2
Perfect score: 1743
Sequence: 1 tccggactagttctagaccg.....aaaaaaaaaaaaaagggcgg 1743

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3340653 seqs, 2534783454 residues

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Post-processing: Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1743	100.0	1743	14	US-10-086-181-1	Sequence 1, Appli
2	1743	100.0	1743	15	US-10-077-698-2	Sequence 2, Appli
3	1743	100.0	1743	15	US-10-171-027-2	Sequence 2, Appli
4	1743	100.0	1743	15	US-10-075-987-2	Sequence 2, Appli
5	1109	63.6	1160	14	US-10-015-498-1	Sequence 1, Appli
6	1086	62.3	1086	14	US-10-086-181-3	Sequence 3, Appli
7	1086	62.3	1086	15	US-10-083-168-11	Sequence 11, Appl
8	1035	59.4	1086	10	US-09-992-331-1	Sequence 1, Appli
9	1035	59.4	1086	15	US-10-083-168-78	Sequence 78, Appl
10	1035	59.4	1086	15	US-10-262-313-1	Sequence 1, Appli
11	1035	59.4	1086	17	US-10-768-878-1	Sequence 1, Appli
12	984	56.5	1086	15	US-10-083-168-80	Sequence 80, Appl
13	926	53.1	1086	9	US-09-995-225-7	Sequence 7, Appli
14	926	53.1	1086	10	US-09-995-225-7	Sequence 7, Appli
15	586	33.6	632	10	US-09-992-331-4	Sequence 4, Appli
16	586	33.6	632	15	US-10-262-313-4	Sequence 4, Appli
17	586	33.6	632	17	US-10-768-878-4	Sequence 4, Appli
18	559	32.1	1066	15	US-10-017-161-1809	Sequence 1809, Ap
19	559	32.1	1066	16	US-10-292-798-1465	Sequence 1465, Ap
20	550	31.6	3173	15	US-10-116-252-5	Sequence 5, Appli
21	391	22.4	1737	15	US-10-225-567A-681	Sequence 681, App
22	337	19.3	388	13	US-10-276-774-265	Sequence 265, App
23	326	18.7	1104	10	US-09-791-932-10	Sequence 10, Appl
24	298	17.1	760	13	US-10-076-555-771	Sequence 771, App
25	198	11.4	300	13	US-10-076-555-45	Sequence 45, Appl
26	143	8.2	300	13	US-10-076-555-46	Sequence 46, Appl
27	131	7.5	638	9	US-09-828-644-58	Sequence 58, Appl
28	111	6.4	426	10	US-09-791-932-33	Sequence 33, Appl
c 29	66	3.8	25871	9	US-09-798-743A-5	Sequence 5, Appli
c 30	65	3.7	178896	17	US-10-450-826-53	Sequence 53, Appl
c 31	58	3.3	2378	13	US-10-027-632-101748	Sequence 101748,
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c 34	58	3.3	162450	15	US-10-126-704-1	Sequence 1, Appli
c 35	57	3.3	80	10	US-09-992-331-5	Sequence 5, Appli
c 36	57	3.3	80	15	US-10-262-313-5	Sequence 5, Appli
c 37	57	3.3	80	17	US-10-768-878-5	Sequence 5, Appli
c 38	57	3.3	19553	9	US-09-764-847-1425	Sequence 1425, Ap
c 39	57	3.3	19553	15	US-10-092-154-1425	Sequence 1425, Ap
c 40	55	3.2	319	17	US-10-474-495-143	Sequence 143, App
c 41	55	3.2	3287	13	US-10-027-632-113282	Sequence 113282,
c 42	55	3.2	3287	13	US-10-027-632-113283	Sequence 113283,
c 43	55	3.2	3287	13	US-10-027-632-113284	Sequence 113284,
c 44	55	3.2	3287	16	US-10-027-632-113282	Sequence 113282,
c 45	55	3.2	3287	16	US-10-027-632-113283	Sequence 113283,

ALIGNMENTS

RESULT 1
US-10-086-181-1
; Sequence 1, Application US/10086181
; Publication No. US20020177151A1
; GENERAL INFORMATION:
; APPLICANT: GIMENO, Ruth
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; TITLE OF INVENTION: DISORDERS, INCLUDING OBESITY AND DIABETES
; FILE REFERENCE: MNI-220
; CURRENT APPLICATION NUMBER: US/10/086,181
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/271,655
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)...(1129)
US-10-086-181-1

Query Match 100.0%; Score 1743; DB 14; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
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Db       301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360

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; Sequence 2, Application US/10077698
; Publication No. US20030008350A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 14273 Receptor, A No. US20030008350A1el G-Protein Coupled Receptor
; FILE REFERENCE: 5800-4B, 035800/177086
; CURRENT APPLICATION NUMBER: US/10/077,698
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/261,599
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/107,761
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-698-2

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
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Qy       901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
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Db       961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
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Db      1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
Qy      1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
Db      1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
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Db      1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
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Qy      1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740
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RESULT 3
US-10-171-027-2
; Sequence 2, Application US/10171027
; Publication No. US20030073168A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: 14273 Receptor, A No. US20030073168A1el G-Protein Coupled Recepto
; FILE REFERENCE: MNI-204CP3
; CURRENT APPLICATION NUMBER: US/10/171,027
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/456,455
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-171-027-2

Query Match 100.0%; Score 1743; DB 15; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120

Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
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Db        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180

Qy        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240
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Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
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Qy        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
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Qy        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
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Db        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480

Qy        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540

Qy        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600

Qy        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660

Qy        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720

Qy        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780

Qy        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840

Qy        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960

Qy        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020

Qy       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080

Qy       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140

Qy       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200

Qy       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260

Qy       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380

Qy       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440

Qy       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500

Qy       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560

Qy       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620

Qy       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680

Qy       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740

Qy       1741 CGG 1743
              |||
Db       1741 CGG 1743
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RESULT 4
US-10-075-987-2
; Sequence 2, Application US/10075987
; Publication No. US20030166061A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 14273 Receptor, A No. US20030166061A1el G-Protein Coupled Receptor
; FILE REFERENCE: 5800-4B, 035800/177086
; CURRENT APPLICATION NUMBER: US/10/075,987
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US/09/261,599B
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-075-987-2

Query Match 100.0%; Score 1743; DB 15; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGC 60
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Qy         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCC 120

Qy        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGT 180

Qy        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGC 240

Qy        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCT 300

Qy        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCT 360

Qy        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCAT 420

Qy        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGG 480

Qy        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTC 540

Qy        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGG 600

Qy        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTC 660

Qy        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAG 720

Qy        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGC 780

Qy        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCT 840

Qy        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCT 900

Qy        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGT 960

Qy        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTG 1020

Qy       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTT 1080

Qy       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTAT 1140

Qy       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGT 1200

Qy       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACCCTCCATCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGC 1260

Qy       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTCGGTAAATTAAGGGGTGATCACCAAGTTTCATAATATTTTCCCTTTATAAAAGGATTT 1320

Qy       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGGAGGCTGAGGTGGGT 1380

Qy       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCCGTCTC 1440

Qy       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TACTAAAAATAAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTA 1500

Qy       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTTGGGAGGCTGAACCAGGAGAATCTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 1560

Qy       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAACTCCATCTTAAAAAAAAA 1620

Qy       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAACTTTTTTAGTGTGTTTGTAATA 1680

Qy       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TGATCAAATTTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAGGG 1740

Qy       1741 CGG 1743
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Db       1741 CGG 1743
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RESULT 5
US-10-015-498-1
; Sequence 1, Application US/10015498
; Publication No. US20020151705A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Quan, Yong
; TITLE OF INVENTION: DNA Encoding Orphan SNORF49 Receptor
; FILE REFERENCE: 60134
; CURRENT APPLICATION NUMBER: US/10/015,498
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US/09/412,933
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-498-1

Query Match 63.6%; Score 1109; DB 14; Length 1160;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         17 ACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCGAC 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCGCTGCGGGCCGCCAGGCGCCGGGAATGTCCCCTGAATGCGCGCGGGCAGCGGGCGAC 60
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Qy         77 GCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACGTC 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCACCCGCTTTCCCTTCTTCTCCGACGTC 120

Qy        137 AAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTT 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGGAGACAACCGTGCTGGTGCTCATCTTT 180

Qy        197 GCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGTGTCGCTGCTGGGCAACGTGTGCGCCCTGGTGCTGGTGGCGCGCCGACGACGCCGC 240

Qy        257 GGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCT 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCGACTGCCTGCCTGGTACTCAACCTCTTCTGCGCGGACCTGCTCTTCATCAGCGCT 300

Qy        317 ATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGC 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGC 360

Qy        377 CACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCG 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CACCTGCTCTTCTACGTGATGACCCTGAGCGGCAGCGTCACCATCCTCACGCTGGCCGCG 420

Qy        437 GTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGG 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCAGCCTGGAGCGCATGGTGTGCATCGTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGG 480

Qy        497 CGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTG 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATCTGGGGCTATTCGGCGGTCGCCGCTCTG 540

Qy        557 CCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAATT 616
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTCTCTGCGTCTTCTTCCGAGTCGTCCCGCAACGGCTCCCCGGCGCCGACCAGGAAATT 600

Qy        617 TCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTT 676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGATTTGCACACTGATTTGGCCCACCATTCCTGGAGAGATCTCGTGGGATGTCTCTTTT 660

Qy        677 GTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTA 736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTTACTTTGAACTTCTTGGTGCCAGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTA 720

Qy        737 CAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCCAC 796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGATCACAAAGGCATCAAGGAAGAGGCTCACGGTAAGCCTGGCCTACTCGGAGAGCCAC 780

Qy        797 CAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGTC 856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCTTCCGCACCCTCTTCCTCCTCATGGTC 840

Qy        857 TCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAAC 916
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTCTTCATCATGTGGAGCCCCATCATCATCACCATCCTCCTCATCCTGATCCAGAAC 900

Qy        917 TTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATTT 976
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCTTCTTCTGGGTGGTGGCCTTCACATTT 960

Qy        977 GCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAAG 1036
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCTAATTCAGCCCTAAACCCCATCCTCTACAACATGACACTGTGCAGGAATGAGTGGAAG 1020

Qy       1037 AAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGTC 1096
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAATTTTTTGCTGCTTCTGGTTCCCAGAAAAGGGAGCCATTTTAACAGACACATCTGTC 1080

Qy       1097 AAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCACA 1156
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAAAGAAATGACTTGTCGATTATTTCTGGCTAATTTTTCTTTATAGCCGAGTTTCTCACA 1140

Qy       1157 CCTGGCGAGCTGTGGCATGC 1176
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Db       1141 CCTGGCGAGCTGTGGCATGC 1160
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RESULT 6
US-10-086-181-3
; Sequence 3, Application US/10086181
; Publication No. US20020177151A1
; GENERAL INFORMATION:
; APPLICANT: GIMENO, Ruth
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; TITLE OF INVENTION: DISORDERS, INCLUDING OBESITY AND DIABETES
; FILE REFERENCE: MNI-220
; CURRENT APPLICATION NUMBER: US/10/086,181
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/271,655
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-086-181-3

Query Match 62.3%; Score 1086; DB 14; Length 1086;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
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Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
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Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
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Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
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Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
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Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
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Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
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Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660
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Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
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Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
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Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
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Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
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Db        841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
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Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
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Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
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Db       1081 GGCTAA 1086
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RESULT 7
US-10-083-168-11
; Sequence 11, Application US/10083168
; Publication No. US20030023069A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Maciejewski-Lenior, Dominique
; APPLICANT: Leonard, James N.
; APPLICANT: Ortuno, Daniel
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0320
; CURRENT APPLICATION NUMBER: US/10/083,168
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-083-168-11

Query Match 62.3%; Score 1086; DB 15; Length 1086;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
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Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
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Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
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Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
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Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
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Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
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Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
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Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
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Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
              ||||||
Db       1081 GGCTAA 1086
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RESULT 8
US-09-992-331-1
; Sequence 1, Application US/09992331
; Publication No. US20030022186A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, JOHN N.

```
;  APPLICANT:  MINTIER, GABE
;  APPLICANT:  RAMANATHAN, CHANDRA S.
;  APPLICANT:  HAWKEN, DONALD R.
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY18,
;  TITLE OF INVENTION:  EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: D0048NP
;  CURRENT APPLICATION NUMBER: US/09/992,331
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/308,540
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/261,782
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: 60/248,483
;  PRIOR FILING DATE: 2000-11-14
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-992-331-1

  Query Match           59.4%;  Score 1035;  DB 10;  Length 1086;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
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Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
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Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

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Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

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Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
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Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

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Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
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Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTCCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
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Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
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Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
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Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

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Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
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Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
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Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
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Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
              ||||||
Db       1081 GGCTAA 1086


RESULT 9
US-10-083-168-78
; Sequence 78, Application US/10083168
; Publication No. US20030023069A1
; GENERAL INFORMATION:
;  APPLICANT: Liaw, Chen W.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Behan, Dominic P.
;  APPLICANT:  Maciejewski-Lenior, Dominique
;  APPLICANT:  Leonard, James N.
;  APPLICANT:  Ortuno, Daniel
;  APPLICANT:  Lin, I-Lin
;  TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Acti
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0320
;  CURRENT APPLICATION NUMBER: US/10/083,168
;  CURRENT FILING DATE:  2002-02-26
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: No. US20030023069A1el Sequence
US-10-083-168-78

  Query Match           59.4%;  Score 1035;  DB 15;  Length 1086;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
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Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
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Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180
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Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
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Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
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Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
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Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
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Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
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Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
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Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
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Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
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Db       1081 GGCTAA 1086
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RESULT 10
US-10-262-313-1
; Sequence 1, Application US/10262313
; Publication No. US20030129653A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY18, EXPRESSED HIGH
;  TITLE OF INVENTION:  PITUITARY GLAND AND COLON CARCINOMA CELLS
;  FILE REFERENCE: D0048 CIP
;  CURRENT APPLICATION NUMBER: US/10/262,313
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: U.S. 09/992,331
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-262-313-1

  Query Match             59.4%;  Score 1035;  DB 15;  Length 1086;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy        104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy        164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy        224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy        284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy        344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy        404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy        524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTCCGAGTCGTC 540

Qy        584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy        644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy        704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy        764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy        824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840
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Qy        884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy        944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy       1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy       1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy       1124 GGCTAA 1129
              ||||||
Db       1081 GGCTAA 1086
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RESULT 11
US-10-768-878-1
; Sequence 1, Application US/10768878
; Publication No. US20040161823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY18, EXPRESSED
; TITLE OF INVENTION: HIGHLY IN PITUITARY GLAND, COLON CARCINOMA, AND LUNG CANCER CELL
; FILE REFERENCE: D0048A CIP2
; CURRENT APPLICATION NUMBER: US/10/768,878
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: U.S. 09/992,331
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/248,483
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: U.S. 10/262,313
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: U.S. 60/261,782
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/308,540
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-768-878-1

Query Match 59.4%; Score 1035; DB 17; Length 1086;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1085; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy         104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy         164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy         224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy         284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy         344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy         404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy         464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy         524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTCCGAGTCGTC 540

Qy         584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy         644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy         704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy         764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy         824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy         884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy         944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy        1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy        1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy        1124 GGCTAA 1129
               ||||||
Db        1081 GGCTAA 1086
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RESULT 12
US-10-083-168-80
; Sequence 80, Application US/10083168
; Publication No. US20030023069A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Maciejewski-Lenior, Dominique
; APPLICANT: Leonard, James N.
; APPLICANT: Ortuno, Daniel
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Acti
; TITLE OF INVENTION: Receptors

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;  FILE REFERENCE: AREN-0320
;  CURRENT APPLICATION NUMBER: US/10/083,168
;  CURRENT FILING DATE:  2002-02-26
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: No. US20030023069A1el Sequence
US-10-083-168-80

  Query Match            56.5%;  Score 984;  DB 15;  Length 1086;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1084;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          44 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 103
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGTCCCCTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCC 60

Qy         104 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 163
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AACCGCACCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCC 120

Qy         164 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 223
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCGGTGGAGACAACCGTGCTGGTGCTCATCTTTGCAGTGTCGCTGCTGGGCAACGTGTGC 180

Qy         224 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 283
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCCCTGGTGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAAC 240

Qy         284 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 343
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTCTTCTGCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGG 300

Qy         344 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 403
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACTGAGGCCTGGCTGCTGGGCCCCGTTGCCTGCCACCTGCTCTTCTACGTGATGACCCTG 360

Qy         404 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 463
               |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Db         361 AGCGGCAGCGTCACCATCCTCACGCTGGCCGCGGTCAGCCTGAATCGCATGGTGTGCATC 420

Qy         464 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 523
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GTGCACCTGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCG 480

Qy         524 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 583
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTCATCTGGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTC 540

Qy         584 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 643
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 CCGCAACGGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACC 600

Qy         644 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 703
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 ATTCCTGGAGAGATCTCGTGGGATGTCTCTTTTGTTACTTTGAACTTCTTGGTGCCAGGA 660

Qy         704 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 763
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGG 720

Qy         764 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 823
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 CTCACGGTAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTC 780

Qy         824 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 883
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 CGGCTCTTCCGCACCCTCTTCCTCCTCATGGTCTCCTTCTTCATCATGTGGAGCCCCATC 840

Qy         884 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 943
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 ATCATCACCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCG 900

Qy         944 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 1003
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TCCCTCTTCTTCTGGGTGGTGGCCTTCACATTTGCTAATTCAGCCCTAAACCCCATCCTC 960

Qy        1004 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1063
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 TACAACATGACACTGTGCAGGAATGAGTGGAAGAAAATTTTTTGCTGCTTCTGGTTCCCA 1020

Qy        1064 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1123
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GAAAAGGGAGCCATTTTAACAGACACATCTGTCAAAAGAAATGACTTGTCGATTATTTCT 1080

Qy        1124 GGCTAA 1129
               ||||||
Db        1081 GGCTAA 1086


RESULT 13
US-09-995-225-7
; Sequence 7, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Ruoping
;  APPLICANT:  Chu, Zhi Liang
;  APPLICANT:  Dang, Huong T.
;  APPLICANT:  Lowitz, Kevin P.
;  APPLICANT:  Pride, Cameron
;  TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0308
;  CURRENT APPLICATION NUMBER: US/09/995,225
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: 60/253,404
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/255,366
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/270,286
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/282,365
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/270,266
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/282,032
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,358
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,356
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/290,917
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: 60/309,208
;  PRIOR FILING DATE: 2001-07-31
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-7

  Query Match            53.1%;  Score 926;  DB 9;  Length 1086;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1076;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Db          8 CTGAATGCGCGCGGGCAGCGGGCGACGCGCCCTTGCGCAGCCTGGAGCAAGCCAACCGCA 67

Qy        111 CCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGG 170
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Db         68 CCCGCTTTCCCTTCTTCTCCGACGTCAAGGGCGACCACCGGCTGGTGCTGGCCGCGGTGG 127

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Db        188 TGCTGGTGGCGCGCCGACGACGCCGCGGCGCGACTGCCTGCCTGGTACTCAACCTCTTCT 247

Qy        291 GCGCGGACCTGCTCTTCATCAGCGCTATCCCTCTGGTGCTGGCCGTGCGCTGGACTGAGG 350
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Db        428 TGCAGCGCGGCGTGCGGGGTCCTGGGCGGCGGGCGCGGGCAGTGCTGCTGGCGCTCATAT 487

Qy        531 GGGGCTATTCGGCGGTCGCCGCTCTGCCTCTCTGCGTCTTCTTTCGAGTCGTCCCGCAAC 590
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Qy        591 GGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTG 650
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Db        548 GGCTCCCCGGCGCCGACCAGGAAATTTCGATTTGCACACTGATTTGGCCCACCATTCCTG 607

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Db        728 TAAGCCTGGCCTACTCGGAGAGCCACCAGATCCGCGTGTCCCAGCAGGACTTCCGGCTCT 787

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Qy        891 CCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCT 950
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; Publication No. US20030139588A9
; GENERAL INFORMATION:
;  APPLICANT: Chen, Ruoping
;  APPLICANT:  Chu, Zhi Liang
;  APPLICANT:  Dang, Huong T.
;  APPLICANT:  Lowitz, Kevin P.
;  APPLICANT:  Pride, Cameron
;  TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0308
;  CURRENT APPLICATION NUMBER: US/09/995,225
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: 60/253,404
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/255,366
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/270,286
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/282,365
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/270,266
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/282,032
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,358
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,356
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/290,917
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: 60/309,208
;  PRIOR FILING DATE: 2001-07-31
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-7

  Query Match           53.1%;  Score 926;  DB 10;  Length 1086;
  Best Local Similarity  99.7%;  Pred. No. 0;
  Matches 1076;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Db        668 TTGTGATCAGTTACTCCAAAATTTTACAGATCACAAAGGCATCAAGGAAGAGGCTCACGG 727

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Qy        891 CCATCCTCCTCATCCTGATCCAGAACTTCAAGCAAGACCTGGTCATCTGGCCGTCCCTCT 950
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; Sequence 4, Application US/09992331
; Publication No. US20030022186A1
; GENERAL INFORMATION:
;  APPLICANT: FEDER, JOHN N.
;  APPLICANT:  MINTIER, GABE
;  APPLICANT:  RAMANATHAN, CHANDRA S.
;  APPLICANT:  HAWKEN, DONALD R.
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY18,
;  TITLE OF INVENTION:  EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: D0048NP
;  CURRENT APPLICATION NUMBER: US/09/992,331
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/308,540
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/261,782
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: 60/248,483
;  PRIOR FILING DATE: 2000-11-14
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 632
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-992-331-4

  Query Match           33.6%;  Score 586;  DB 10;  Length 632;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-277;
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Job time : 823.411 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 19:03:02 ; Search time 5921.2 Seconds
(without alignments)
11419.163 Million cell updates/sec

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Perfect score: 1560
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: gb_htg:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	1560	100.0	1560	6	BD269631	BD269631 14273 rec
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	4	1560	100.0	1560	6	AR372102	AR372102 Sequence
	5	947	60.7	1419	10	BC053698	BC053698 Mus muscu
	6	744	47.7	1086	10	AY288424	AY288424 Mus muscu
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	8	596	38.2	239718	2	AC101774	AC101774 Mus muscu
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	10	138	8.8	138	6	AR228219	AR228219 Sequence
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	15	77	4.9	225030	10	AC107608	AC107608 Rattus no
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c	17	77	4.9	249741	2	AC096330	AC096330 Rattus no
	18	77	4.9	271367	2	AC105467	AC105467 Rattus no
c	19	77	4.9	271995	2	AC080155	AC080155 Rattus no
	20	57	3.7	238070	2	AC134313	AC134313 Rattus no
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	29	44	2.8	1737	6	AX549396	AX549396 Sequence
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	34	42	2.7	933	6	AX657504	AX657504 Sequence
	35	40	2.6	1066	6	AX647273	AX647273 Sequence
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c	45	38	2.4	762	6	BD079639	BD079639 Cancer-as

ALIGNMENTS

RESULT 1
BD240721
LOCUS BD240721 1560 bp DNA linear PAT 17-JUL-2003
DEFINITION 14273 receptor, a G-protein coupled receptor.
ACCESSION BD240721
VERSION BD240721.1 GI:33050491
KEYWORDS JP 2002522011-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Glucksmann,M.A. and Tsai,F.Y.
TITLE 14273 receptor, a G-protein coupled receptor
JOURNAL Patent: JP 2002522011-A 2 23-JUL-2002;
MILLENNIUM PHARMACEUTICALS INC

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COMMENT     OS   Murine ortholog
            PN   JP 2002522011-A/2
            PD   23-JUL-2002
            PF   30-JUN-1999 JP 2000557364
            PR   30-JUN-1998 US    09/107761,30-DEC-1998 US    09/223538 PR
            26-FEB-1999 US    09/261599
            PI   MARIA ALEXANDRA GLUCKSMANN,FONG YING TSAI
            PC   C12N15/09,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53//C12P21/08,
            PC   C12N15/00,
            PC   C12N5/00
            CC   14273 receptor, a G-protein coupled receptor
            FH   Key             Location/Qualifiers
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            FT                   /organism='Murine ortholog'.
FEATURES              Location/Qualifiers
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ORIGIN

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  Matches 1560;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
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Qy        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
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Db       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260

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RESULT 2
BD269631
LOCUS       BD269631               1560 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  14273 receptor, a novel G-protein coupled receptor.
ACCESSION   BD269631
VERSION     BD269631.1  GI:33079399
KEYWORDS    JP 2002536997-A/2.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Glucksmann,M.A. and Tsai,F.Y.
  TITLE     14273 receptor, a novel G-protein coupled receptor
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  JOURNAL   Patent: JP 2002536997-A 2 05-NOV-2002;
            MILLENNIUM PHARMACEUTICALS INC
COMMENT     OS   Mus sp. (murine)
            PN   JP 2002536997-A/2
            PD   05-NOV-2002
            PF   28-FEB-2000 JP 2000601160
            PR   26-FEB-1999 US    09/261599,08-DEC-1999 US    09/456455 PI
            MARIA ALEXANDRA GLUCKSMANN,FONG YING TSAI
            PC   C12N15/09,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
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            PC   C12N15/00,
            PC   C12N5/00
            CC   Murine ortholog
            FH   Key             Location/Qualifiers
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ORIGIN

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  Matches 1560;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560


RESULT 3
AR228217
LOCUS       AR228217                1560 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6448005.
ACCESSION   AR228217
VERSION     AR228217.1  GI:27266964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Glucksmann,M.A. and Tsai,F.-Y.
  TITLE     14723 Receptor, a novel G-protein coupled receptor
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  JOURNAL   Patent: US 6448005-A 5 10-SEP-2002;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
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Qy        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600
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Qy        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840

Qy        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900

Qy        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960

Qy        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020
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Db        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
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Db       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200

Qy       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260
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Qy       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320
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Db       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320

Qy       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
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Db       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380

Qy       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440

Qy       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500

Qy       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
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Db       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560


RESULT 4
AR372102
LOCUS       AR372102                1560 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 5 from patent US 6395877.
ACCESSION   AR372102
VERSION     AR372102.1  GI:34609379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Glucksmann,M.A. and Tsai,F.-Y.
  TITLE     14273 receptor, a novel G-protein coupled receptor
  JOURNAL   Patent: US 6395877-A 5 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .1560
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ORIGIN

  Query Match           100.0%;  Score 1560;  DB 6;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1560;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60

Qy         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
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Db        61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
Qy       121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
Db       121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
Qy       181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
Db       181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
Qy       241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
Db       241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
Qy       301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
Db       301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
Qy       361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
Db       361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
Qy       421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
Db       421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
Qy       481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
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Qy       541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600
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Qy       601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660
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Qy       661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720
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Qy       721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
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Qy       781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840
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Qy       841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
Db       841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
Qy       901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
Db       901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
Qy       961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020
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Qy      1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
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Qy      1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
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Qy      1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
Db      1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
Qy      1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260
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Qy      1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
Db      1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
Qy      1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
Db      1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
Qy      1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
Db      1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
Qy      1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
Db      1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
```

RESULT 5
BC053698
LOCUS BC053698 1419 bp mRNA linear ROD 12-NOV-2003
DEFINITION Mus musculus G protein-coupled receptor 120, mRNA (cDNA clone MGC:62870 IMAGE:6529120), complete cds.
ACCESSION BC053698
VERSION BC053698.1 GI:31566089
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1419)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1419)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
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            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 116 Row: n Column: 18.
FEATURES             Location/Qualifiers
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     CDS             49. .1134
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                     family)"
                     /db_xref="CDD:pfam00001"
ORIGIN

  Query Match             60.7%;  Score 947;  DB 10;  Length 1419;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 1247;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 144

Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
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Qy        411 GCGTCAGCCAGCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATC 470
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Qy        531 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 590
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Qy        711 CTCTACATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 770
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Qy        771 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAG 830
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Qy        831 ACTTTGAACTTCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAG 890
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Qy        891 ATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAG 950
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Qy        951 ATCCGAGTGTCCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCC 1010
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Qy       1011 TTCTTCATCATGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTC 1070
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Qy       1071 CGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCC 1130
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Db        925 CGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCC 984

Qy       1131 AACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAG 1190
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Db        985 AACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAG 1044

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Qy       1311 TGCATGTAAAGGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATAC 1370
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Qy       1431 AAAATATTTTTCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTT 1483
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RESULT 6
AY288424
LOCUS       AY288424                1086 bp    mRNA    linear   ROD 08-DEC-2003
DEFINITION  Mus musculus G protein-coupled receptor 120 (Gpr120) mRNA, complete
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ACCESSION   AY288424
VERSION     AY288424.1  GI:32165531
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1086)
  AUTHORS   Fredriksson,R., Hoglund,P.J., Gloriam,D.E., Lagerstrom,M.C. and
            Schioth,H.B.
  TITLE     Seven evolutionarily conserved human rhodopsin G protein-coupled
            receptors lacking close relatives
  JOURNAL   FEBS Lett. 554 (3), 381-388 (2003)
  MEDLINE   22985413
   PUBMED   14623098
REFERENCE   2  (bases 1 to 1086)
  AUTHORS   Fredriksson,R., Hoglund,P.J., Gloriam,D.E.I., Lagerstrom,M.C. and
            Schioth,H.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-2003) Neuroscience; Unit of Pharmacology, Uppsala
            University, Box 593, Uppsala 75124, Sweden
FEATURES             Location/Qualifiers
     source          1. .1086
                     /organism="Mus musculus"
                     /mol_type="mRNA"
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     gene            1. .1086
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ORIGIN

  Query Match           47.7%;  Score 744;  DB 10;  Length 1086;
  Best Local Similarity  99.4%;  Pred. No. 0;
  Matches 1044;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        231 CCCTCGCACACCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAG 290
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Qy        291 GGCGACCACCGGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTC 350
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Qy        471 CCTCTAGTGCTCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCAC 530
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Qy        531 CTGCTCTTCTACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTC 590
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Qy        591 AGCCTGGAGCGCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGG 650
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Db        457 CGGACTCAGGCGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCC 516

Qy        711 CTCTACATCTTGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCG 770
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Qy        771 ATTTGCACATTGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAG 830
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Qy        951 ATCCGAGTGTCCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCC 1010
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Qy       1071 CGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCC 1130
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Qy       1131 AACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAG 1190
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Qy       1191 ATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGG 1250
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RESULT 7
AC112153/c
LOCUS       AC112153               180944 bp    DNA     linear   ROD 27-NOV-2003
DEFINITION  Mus musculus BAC clone RP24-93G11 from chromosome 19, complete
            sequence.
ACCESSION   AC112153
VERSION     AC112153.4  GI:34495034
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 180944)
  AUTHORS   Tomlinson,C. and Haglund,K.
  TITLE     The sequence of Mus musculus BAC clone RP24-93G11
  JOURNAL   Unpublished (2001)
REFERENCE   2  (bases 1 to 180944)
  AUTHORS   Wilson,R.
  TITLE     Sequencing of Mus musculus
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 180944)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-FEB-2002) Genome Sequencing Center, 4444 Forest Park
```

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            Parkway, St. Louis, MO 63108, USA
REFERENCE   4  (bases 1 to 180944)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2003) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   5  (bases 1 to 180944)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-SEP-2003) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   6  (bases 1 to 180944)
  AUTHORS   Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-NOV-2003) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Sep 6, 2003 this sequence version replaced gi:30725984.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu
                Contact: submissions@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: M_BB0093G11
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. Wes Warren,
            Department of Genetics, Washington University, St. Louis MO. For
            additional information about the map position of this sequence, see
            http://genome.wustl.edu

            SOURCE INFORMATION:
            The RPCI-24 BAC Library has been constructed by Pieter de Jong and
            coworkers (http://www.chori.org) from male C57BL/6J mouse spleen
            and/or brain genomic DNA. The clone and detailed information can be
            obtained from Pieter de Jong and coworkers at http://www.chori.org

            NEIGHBORING SEQUENCE INFORMATION:
            This sequence is the entire insert of the clone.
FEATURES             Location/Qualifiers
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Qy        888 CAGATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCAC 947
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Qy        948 CAGATCCGAGTGTCCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTT 1007
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Qy       1068 TTCCGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTT 1127
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Db     151798 TTCCGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTT 151739

Qy       1128 GCCAACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGG 1187
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Db     151738 GCCAACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGG 151679

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Db     151678 AAGATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTC 151619

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Qy       1308 GTGTGCATGTAAAGGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAA 1367
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Qy       1368 TACCCGACTTCCAACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGT 1427
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Qy       1428 ATAAAAATATTTTTCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTT 1483
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Db     151438 ATAAAAATATTTTTCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTT 151383


RESULT 8
AC101774
LOCUS       AC101774               239718 bp    DNA     linear   HTG 09-JUN-2003
DEFINITION  Mus musculus clone RP24-113J17, WORKING DRAFT SEQUENCE, 20
            unordered pieces.
ACCESSION   AC101774
VERSION     AC101774.3  GI:31544114
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 239718)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus, clone RP24-113J17
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 239718)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
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            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 239718)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
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            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jun 9, 2003 this sequence version replaced gi:22380786.
            All repeats were identified using RepeatMasker:
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            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L17381
                Center clone name: 113_J_17
            -------------- Summary Statistics
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                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 233359 bases at least Q40
                Consensus quality: 235646 bases at least Q30
                Consensus quality: 236645 bases at least Q20
                Insert size: 210000; agarose-fp
                Insert size: 237818; sum-of-contigs
                Quality coverage: 9.1 in Q20 bases; agarose-fp
                Quality coverage: 8.1 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 20 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1      309: contig of 309 bp in length
            *      310      409: gap of 100 bp
            *      410     1476: contig of 1067 bp in length
            *     1477     1576: gap of 100 bp
            *     1577     2753: contig of 1177 bp in length
            *     2754     2853: gap of 100 bp
            *     2854     3880: contig of 1027 bp in length
            *     3881     3980: gap of 100 bp
            *     3981     5036: contig of 1056 bp in length
            *     5037     5136: gap of 100 bp
            *     5137     6296: contig of 1160 bp in length
            *     6297     6396: gap of 100 bp
            *     6397     7884: contig of 1488 bp in length
            *     7885     7984: gap of 100 bp
            *     7985     9674: contig of 1690 bp in length
            *     9675     9774: gap of 100 bp
            *     9775    10981: contig of 1207 bp in length
            *    10982    11081: gap of 100 bp
            *    11082    13247: contig of 2166 bp in length
            *    13248    13347: gap of 100 bp
            *    13348    16734: contig of 3387 bp in length
            *    16735    16834: gap of 100 bp
            *    16835    23539: contig of 6705 bp in length
            *    23540    23639: gap of 100 bp
            *    23640    29386: contig of 5747 bp in length
            *    29387    29486: gap of 100 bp
            *    29487    43815: contig of 14329 bp in length
            *    43816    43915: gap of 100 bp
            *    43916    55354: contig of 11439 bp in length
            *    55355    55454: gap of 100 bp
            *    55455    82497: contig of 27043 bp in length
            *    82498    82597: gap of 100 bp
            *    82598   109798: contig of 27201 bp in length
            *   109799   109898: gap of 100 bp
            *   109899   181806: contig of 71908 bp in length
            *   181807   181906: gap of 100 bp
            *   181907   213173: contig of 31267 bp in length
            *   213174   213273: gap of 100 bp
            *   213274   239718: contig of 26445 bp in length.
FEATURES             Location/Qualifiers
     source          1. .239718
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="RP24-113J17"
                     /clone_lib="RPCI-24 Male Mouse BAC"
     misc_feature    1. .309
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     misc_feature    410. .1476
                     /note="assembly_fragment"
     misc_feature    1577. .2753
                     /note="assembly_fragment"
     misc_feature    2854. .3880
                     /note="assembly_fragment"
     misc_feature    3981. .5036
                     /note="assembly_fragment"
     misc_feature    5137. .6296
                     /note="assembly_fragment"
     misc_feature    6397. .7884
                     /note="assembly_fragment"
     misc_feature    7985. .9674
                     /note="assembly_fragment"
     misc_feature    9775. .10981
                     /note="assembly_fragment"
     misc_feature    11082. .13247
                     /note="assembly_fragment"
     misc_feature    13348. .16734
                     /note="assembly_fragment"
     misc_feature    16835. .23539
                     /note="assembly_fragment"
     misc_feature    23640. .29386
                     /note="assembly_fragment"
     misc_feature    29487. .43815
                     /note="assembly_fragment"
     misc_feature    43916. .55354
                     /note="assembly_fragment"
     misc_feature    55455. .82497
                     /note="assembly_fragment"
     misc_feature    82598. .109798
                     /note="assembly_fragment"
     misc_feature    109899. .181806
                     /note="assembly_fragment"
     misc_feature    181907. .213173
                     /note="assembly_fragment"
     misc_feature    213274. .239718
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
ORIGIN

  Query Match             38.2%;  Score 596;  DB 2;  Length 239718;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  596;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        888 CAGATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCAC 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100558 CAGATCACGAAAGCATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCAC 100617

Qy        948 CAGATCCGAGTGTCCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTT 1007
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100618 CAGATCCGAGTGTCCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTT 100677

Qy       1008 TCCTTCTTCATCATGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAAC 1067
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100678 TCCTTCTTCATCATGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAAC 100737

Qy       1068 TTCCGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTT 1127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100738 TTCCGGCAGGACCTGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTT 100797

Qy       1128 GCCAACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGG 1187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100798 GCCAACTCTGCCCTAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGG 100857
```

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Qy       1188 AAGATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTC 1247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100858 AAGATTTTTTGCTGCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTC 100917

Qy       1248 AGGCGAAATGACTTGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACG 1307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100918 AGGCGAAATGACTTGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACG 100977

Qy       1308 GTGTGCATGTAAAGGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAA 1367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100978 GTGTGCATGTAAAGGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAA 101037

Qy       1368 TACCCGACTTCCAACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGT 1427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101038 TACCCGACTTCCAACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGT 101097

Qy       1428 ATAAAAATATTTTTCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTT 1483
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101098 ATAAAAATATTTTTCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTT 101153
```

RESULT 9
AR228218
LOCUS AR228218 181 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 14 from patent US 6448005.
ACCESSION AR228218
VERSION AR228218.1 GI:27266965
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 181)
AUTHORS Glucksmann,M.A. and Tsai,F.-Y.
TITLE 14723 Receptor, a novel G-protein coupled receptor
JOURNAL Patent: US 6448005-A 14 10-SEP-2002;
FEATURES Location/Qualifiers
source 1. .181
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 11.6%; Score 181; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.7e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 60

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 120

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 180

Qy       1201 G 1201
             |
Db        181 G 181
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RESULT 10
AR228219
LOCUS AR228219 138 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 15 from patent US 6448005.
ACCESSION AR228219
VERSION AR228219.1 GI:27266966
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 138)
AUTHORS Glucksmann,M.A. and Tsai,F.-Y.
TITLE 14723 Receptor, a novel G-protein coupled receptor
JOURNAL Patent: US 6448005-A 15 10-SEP-2002;
FEATURES Location/Qualifiers
source 1. .138
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 8.8%; Score 138; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 4.9e-69;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        909 AAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAA 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAA 60

Qy        969 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 120

Qy       1029 CCCATCATCATCACCATC 1046
              ||||||||||||||||||
Db        121 CCCATCATCATCACCATC 138
```

RESULT 11
BC049237/c
LOCUS BC049237 835 bp mRNA linear ROD 07-OCT-2003
DEFINITION Mus musculus electron transferring flavoprotein, beta polypeptide, mRNA (cDNA clone MGC:54845 IMAGE:4241552), complete cds.
ACCESSION BC049237
VERSION BC049237.1 GI:29351580
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 835)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 835)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 99 Row: c Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES Location/Qualifiers
source 1. .835
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="MGC:54845 IMAGE:4241552"
/tissue_type="Kidney, normal. 5 month old male mouse."
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
gene 1. .835
/gene="Etfb"
/db_xref="LocusID:110826"
/db_xref="MGI:106098"
CDS 6. .773
/codon_start=1
/product="Etfb protein"
/protein_id="AAH49237.1"
/db_xref="GI:29351581"
/db_xref="LocusID:110826"
/translation="MAELRALVAVKRVIDFAVKIRVKPDKSGVVTDGVKHSMNPFCEI
AVEEAVRLKEKKLVKEIIAVSCGPSQCQETIRTALAMGADRGIHVEIPGAQAESLGPL
QVARVLAKLAEKEKVDLLFLGKQAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKV
KVEREIDGGLETLRLKLPAVVTADLRLNEPRYATLPNIMKAKKKKIEVVKAGDLGVDL
TSKVSVISVEEPPQRSAGVKVETTEDLVAKLKEVGRI"
misc_feature 15. .758
/note="ETF_beta; Region: Electron transfer flavoprotein beta subunit. This protein is distantly related to and forms a heterodimer with pfam00766"
/db_xref="CDD:pfam01012"

ORIGIN

Query Match 6.5%; Score 101; DB 10; Length 835;
Best Local Similarity 99.3%; Pred. No. 3.7e-47;
Matches 151; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          18 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTGAC 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         152 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTGAC 93

Qy          78 CACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAGTCGATGACCCTCTTGAC 137
               |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          92 CACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGAAGTCGATGACCCTCTTGAC 33

Qy         138 AGCCACGAGCGCGCGCAGCTCCGCCATCTTCC 169
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Db          32 AGCCACGAGCGCGCGCAGCTCCGCCATCTTCC 1
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RESULT 12

AC123550/c
LOCUS AC123550 169206 bp DNA linear ROD 27-NOV-2003
DEFINITION Mus musculus BAC clone RP24-289C13 from chromosome 7, complete sequence.
ACCESSION AC123550
VERSION AC123550.5 GI:30985125
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 169206)
AUTHORS Bielicki,L.
TITLE The sequence of Mus musculus BAC clone RP24-289C13
JOURNAL Unpublished (2001)
REFERENCE 2 (bases 1 to 169206)
AUTHORS Wilson,R.
TITLE Sequencing of Mus musculus
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 169206)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 169206)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 169206)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 169206)
AUTHORS Wilson,R.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On May 22, 2003 this sequence version replaced gi:27531875.
---------- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
---------- Summary Statistics
Center project name: M_BB0289C13
----------.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

SOURCE INFORMATION:
The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

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          NEIGHBORING SEQUENCE INFORMATION:
          This sequence is the entire insert of the clone.
FEATURES             Location/Qualifiers
     source          1. .169206
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="7"
                     /map="7"
                     /clone="RP24-289C13"
                     /clone_lib="RPCI-24"
     repeat_region   1. .90
                     /rpt_family="B2"
     repeat_region   398. .548
                     /rpt_family="Alu"
     repeat_region   1705. .1784
                     /rpt_family="MIR"
     repeat_region   2903. .3072
                     /rpt_family="B4"
     repeat_region   3609. .4021
                     /rpt_family="MaLR"
     repeat_region   6106. .6248
                     /rpt_family="Alu"
     repeat_region   7008. .7052
                     /rpt_family="ERV1"
     repeat_region   7053. .7205
                     /rpt_family="B4"
     repeat_region   7206. .7343
                     /rpt_family="ERV1"
     repeat_region   7504. .7773
                     /rpt_family="L1"
     repeat_region   7804. .8139
                     /rpt_family="MaLR"
     repeat_region   8217. .8597
                     /rpt_family="MaLR"
     repeat_region   8598. .8652
                     /rpt_family="L1"
     repeat_region   8621. .9123
                     /rpt_family="L1"
     repeat_region   9159. .9275
                     /rpt_family="L1"
     repeat_region   9288. .9434
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     repeat_region   9648. .9807
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     repeat_region   9813. .9956
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     repeat_region   9958. .10577
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     repeat_region   11055. .11618
                     /rpt_family="L1"
     repeat_region   11619. .11840
                     /rpt_family="B2"
     repeat_region   11841. .12020
                     /rpt_family="L1"
     repeat_region   13831. .13978
                     /rpt_family="L1"
     repeat_region   13979. .14312
                     /rpt_family="MaLR"
     repeat_region   14317. .14730
                     /rpt_family="L1"
     repeat_region   14731. .14915
                     /rpt_family="B2"
     repeat_region   14916. .14967
                     /rpt_family="L1"
     repeat_region   16136. .16585
                     /rpt_family="L1"
     repeat_region   17108. .18100
                     /rpt_family="L1"
     unsure          18285. .18307
                     /note="Sequence derived from one plasmid subclone."
     repeat_region   18359. .18501
                     /rpt_family="Alu"
     repeat_region   18511. .19194
                     /rpt_family="L1"
     repeat_region   19246. .19380
                     /rpt_family="B2"
     repeat_region   19381. .19425
                     /rpt_family="B4"
     repeat_region   19600. .19790
                     /rpt_family="B2"
     repeat_region   19869. .20088
                     /rpt_family="B4"
     repeat_region   20115. .20270
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     repeat_region   20581. .20778
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     repeat_region   21094. .21186
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     repeat_region   21228. .21307
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     repeat_region   21499. .21743
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     repeat_region   21822. .22007
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     repeat_region   22126. .22216
                     /rpt_family="B4"
     repeat_region   23839. .24140
                     /rpt_family="L1"
     repeat_region   25383. .25460
                     /rpt_family="ID"
     tRNA            25388. .25456
                     /product="tRNA-Ala"
                     /note="Likely pseudogene (HMM Sc=34.12 / Sec struct
                     Sc=1.92)"
     repeat_region   26997. .27316
                     /rpt_family="ERVL"
     repeat_region   27476. .27572
                     /rpt_family="Alu"
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  Query Match             5.9%;  Score 92;  DB 10;  Length 169206;
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Qy         18 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTGAC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80518 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTGAC 80459

Qy         78 CACTCCAGACTTGTCCGGCTTTACCCGAATCT 109
              |||||||||||||||||||||||||||||||
Db      80458 CACTCCAGACTTGTCCGGCTTTACCCGAATCT 80427


RESULT 13
AC079543
LOCUS       AC079543              277603 bp    DNA     linear   HTG 02-SEP-2000
DEFINITION  Mus musculus clone RP23-381P16, WORKING DRAFT SEQUENCE, 67
```

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            unordered pieces.
ACCESSION   AC079543
VERSION     AC079543.1  GI:9964908
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 277603)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Mouse
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 277603)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     -------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -------
            Project Information
            Center Project Name: 1883552
            Center clone name: RPCI-23_381P16
            -------
            Summary Statistics
            Consensus quality: 224010 bases at least Q40
            Consensus quality: 249280 bases at least Q30
            Consensus quality: 255396 bases at least Q20
            Estimated insert size: 172000; agarose-fp estimation
            Estimated insert size: 271003; sum-of-contigs estimation
            Quality coverage:  6.92 in Q20 bases; agarose-fp estimation
            Quality coverage:  4.39 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 67 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1043: contig of 1043 bp in length
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            *     1144     2187: contig of 1044 bp in length
            *     2188     2287: gap of unknown length
            *     2288     3468: contig of 1181 bp in length
            *     3469     3568: gap of unknown length
            *     3569     4840: contig of 1272 bp in length
            *     4841     4940: gap of unknown length
            *     4941     6012: contig of 1072 bp in length
            *     6013     6112: gap of unknown length
            *     6113     7304: contig of 1192 bp in length
            *     7305     7404: gap of unknown length
            *     7405     8702: contig of 1298 bp in length
            *     8703     8802: gap of unknown length
            *     8803    10001: contig of 1199 bp in length
            *    10002    10101: gap of unknown length
            *    10102    11249: contig of 1148 bp in length
            *    11250    11349: gap of unknown length
            *    11350    12629: contig of 1280 bp in length
            *    12630    12729: gap of unknown length
            *    12730    13945: contig of 1216 bp in length
            *    13946    14045: gap of unknown length
            *    14046    15833: contig of 1788 bp in length
            *    15834    15933: gap of unknown length
            *    15934    17862: contig of 1929 bp in length
            *    17863    17962: gap of unknown length
            *    17963    18991: contig of 1029 bp in length
            *    18992    19091: gap of unknown length
            *    19092    20898: contig of 1807 bp in length
            *    20899    20998: gap of unknown length
            *    20999    22832: contig of 1834 bp in length
            *    22833    22932: gap of unknown length
            *    22933    24144: contig of 1212 bp in length
            *    24145    24244: gap of unknown length
            *    24245    25669: contig of 1425 bp in length
            *    25670    25769: gap of unknown length
            *    25770    27239: contig of 1470 bp in length
            *    27240    27339: gap of unknown length
            *    27340    28790: contig of 1451 bp in length
            *    28791    28890: gap of unknown length
            *    28891    30106: contig of 1216 bp in length
            *    30107    30206: gap of unknown length
            *    30207    31602: contig of 1396 bp in length
            *    31603    31702: gap of unknown length
            *    31703    32867: contig of 1165 bp in length
            *    32868    32967: gap of unknown length
            *    32968    34416: contig of 1449 bp in length
            *    34417    34516: gap of unknown length
            *    34517    35577: contig of 1061 bp in length
            *    35578    35677: gap of unknown length
            *    35678    37248: contig of 1571 bp in length
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            *    37349    38610: contig of 1262 bp in length
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            *    48710    49895: contig of 1186 bp in length
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            *    49996    51506: contig of 1511 bp in length
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            *    53109    55140: contig of 2032 bp in length
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            *    55241    57760: contig of 2520 bp in length
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            *    57861    59903: contig of 2043 bp in length
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            *    60004    62375: contig of 2372 bp in length
            *    62376    62475: gap of unknown length
            *    62476    64891: contig of 2416 bp in length
            *    64892    64991: gap of unknown length
            *    64992    67699: contig of 2708 bp in length
            *    67700    67799: gap of unknown length
            *    67800    69624: contig of 1825 bp in length
            *    69625    69724: gap of unknown length
            *    69725    71722: contig of 1998 bp in length
            *    71723    71822: gap of unknown length
            *    71823    75072: contig of 3250 bp in length
            *    75073    75172: gap of unknown length
            *    75173    77256: contig of 2084 bp in length
            *    77257    77356: gap of unknown length
            *    77357    79802: contig of 2446 bp in length
            *    79803    79902: gap of unknown length
            *    79903    81721: contig of 1819 bp in length
            *    81722    81821: gap of unknown length
            *    81822    86203: contig of 4382 bp in length
            *    86204    86303: gap of unknown length
            *    86304    92047: contig of 5744 bp in length
            *    92048    92147: gap of unknown length
            *    92148    95857: contig of 3710 bp in length
            *    95858    95957: gap of unknown length
            *    95958    99755: contig of 3798 bp in length
            *    99756    99855: gap of unknown length
```

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            *   119953   120052: gap of unknown length
            *   120053   121219: contig of 1167 bp in length
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            *   121320   129289: contig of 7970 bp in length
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            *   129390   139138: contig of 9749 bp in length
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            *   162417   174418: contig of 12002 bp in length
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            *   174519   192093: contig of 17575 bp in length
            *   192094   192193: gap of unknown length
            *   192194   212136: contig of 19943 bp in length
            *   212137   212236: gap of unknown length
            *   212237   233430: contig of 21194 bp in length
            *   233431   233530: gap of unknown length
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ORIGIN

  Query Match             5.9%;  Score 92;  DB 2;  Length 277603;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-41;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTGAC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250130 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTGAC 250189

Qy         78 CACTCCAGACTTGTCCGGCTTTACCCGAATCT 109
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Db     250190 CACTCCAGACTTGTCCGGCTTTACCCGAATCT 250221


RESULT 14
AC080156
LOCUS       AC080156               212822 bp    DNA     linear   HTG 09-OCT-2002
DEFINITION  Rattus norvegicus clone RP32-379B20, *** SEQUENCING IN PROGRESS
            ***, 8 unordered pieces.
ACCESSION   AC080156
VERSION     AC080156.9  GI:23269308
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 212822)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
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            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 212822)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-SEP-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 212822)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-OCT-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 23, 2002 this sequence version replaced gi:21953772.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequening reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/).  As a result, the
            sequence may extend beyond the ends of the clone and there may be
            contigs that consist entirely of whole genome shotgun sequence
            reads.  Both end sequences and whole genome shotgun sequence only
            contigs will be indicated in the feature table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: TUAB
                Center clone name: RP32-379B20
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 196316 bases at least Q40
                Consensus quality: 197975 bases at least Q30
                Consensus quality: 199394 bases at least Q20
                Estimated insert size: 222120; sum-of-contigs estimation
                Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
```

```
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *  205472   206631: contig of 1160 bp in length
            *  206632   206731: gap of unknown length
            *  206732   207869: contig of 1138 bp in length
            *  207870   207969: gap of unknown length
            *  207970   209084: contig of 1115 bp in length
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ORIGIN

  Query Match             4.9%;  Score 77;  DB 2;  Length 212822;
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Qy        987 ACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCATCATCATCACCATC 1046
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Db     114483 ACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCATCATCATCACCATC 114542

Qy       1047 CTCCTCATCTTGATCCA 1063
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Db     114543 CTCCTCATCTTGATCCA 114559


RESULT 15
AC107608
LOCUS       AC107608               225030 bp    DNA     linear   ROD 30-JUL-2003
DEFINITION  Rattus norvegicus 1 BAC CH230-204P6 (Children's Hospital Oakland
            Research Institute) complete sequence.
ACCESSION   AC107608
VERSION     AC107608.6  GI:33342287
KEYWORDS    HTG.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 225030)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
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            Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,
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            Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
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            Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
            Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 225030)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 225030)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   4  (bases 1 to 225030)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUL-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jul 30, 2003 this sequence version replaced gi:25072936.
            Sequencing is completed to a minimum standard of double strand
            coverage with a minimum of 2 clones and 2 reads with no ambiguities
            or 2 chemistries with a minimum of 2 clones and 3 reads with no
            ambiguities. If the sequence quality does not meet this standard,
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 19:01:32 ; Search time 569.119 Seconds
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Title: US-10-077-698-5
Perfect score: 1560
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1212	77.7	1561	3	AAZ49746	Aaz49746 Murine 14
4	180	11.5	180	3	AAA64344	Aaa64344 Probe for
5	138	8.8	138	3	AAA64345	Aaa64345 Probe for
6	44	2.8	1086	6	ABT04869	Abt04869 Human G p
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8	44	2.8	1086	6	ABS73399	Abs73399 DNA encod
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21	40	2.6	1104	4	AAS42815	Aas42815 Human G P
22	40	2.6	3173	4	AAC82670	Aac82670 Human 7TM
23	39	2.5	638	6	AAS62901	Aas62901 Human G p
24	38	2.4	241	3	AAZ80388	Aaz80388 Human col
c 25	38	2.4	459	8	ACH44239	Ach44239 Human foe
c 26	38	2.4	472	8	ACH40136	Ach40136 Human foe
c 27	38	2.4	487	3	AAC02281	Aac02281 Human sec
c 28	38	2.4	489	8	ACH45264	Ach45264 Human foe
c 29	38	2.4	490	8	ACH13024	Ach13024 Human adu
30	38	2.4	500	5	ABV60845	Abv60845 Human pro
c 31	38	2.4	517	8	ACH43949	Ach43949 Human foe
c 32	38	2.4	762	2	AAX39905	Aax39905 Gastric c
c 33	38	2.4	768	6	ABL39413	Abl39413 Human ele
c 34	38	2.4	813	2	AAX39904	Aax39904 Gastric c
c 35	38	2.4	912	5	AAS70364	Aas70364 DNA encod
c 36	38	2.4	919	3	AAC98786	Aac98786 Human pan
c 37	38	2.4	930	5	AAS70067	Aas70067 DNA encod
c 38	38	2.4	1281	7	ADA52753	Ada52753 Human cod
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c 40	38	2.4	29222	6	ABL39412	Abl39412 Human ele
c 41	29	1.9	469	8	ACH45354	Ach45354 Human foe
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ALIGNMENTS

RESULT 1
AAA64347
ID AAA64347 standard; DNA; 1560 BP.
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AC AAA64347;
XX
DT 20-DEC-2000 (first entry)
XX
DE DNA encoding a murine G-protein coupled receptor designated 14273.
XX
KW Mouse; G-protein coupled receptor; receptor-mediated disorder;
KW 14273 receptor; cardiovascular disease; congestive heart failure;
KW cardiac myocyte hypertrophy; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 195. .1280
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PN WO200050596-A2.
XX
PD 31-AUG-2000.
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PF 28-FEB-2000; 2000WO-US005068.
XX
PR 26-FEB-1999; 99US-00261599.
PR 08-DEC-1999; 99US-00456455.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Glucksmann MA, Tsai F;
XX
DR WPI; 2000-587184/55.
DR P-PSDB; AAB08539.
XX
PT 14273 receptor polynucleotides and polypeptides, useful in the diagnosis
PT and treatment of receptor-mediated disorders such as cardiovascular
PT diseases.
XX
PS Claim 3; Fig 7; 105pp; English.
XX
CC The present sequence encodes a murine G-protein coupled receptor,
CC designated 14273 receptor. The G-protein coupled receptor 14273
CC polypeptide is used to produce antibodies, in drug screening assays, and

```
CC   to screen for agonist and antagonists. The antibodies are used for
CC   diagnostic applications, and to assess abnormal tissue distributions or
CC   abnormal expression during development. The antibodies are also useful
CC   for tissue typing, and in forensic identification, as well as for
CC   inhibiting receptor function. The 14273 polynucleotides can be used to
CC   express the protein, to detect 14273 mRNA, to detect genetic alterations
CC   in the 14273 gene, and as a source of primers and probes. The 14273
CC   polynucleotides and polypeptides are also useful as a target for
CC   diagnosis and treatment of receptor-mediated disorders, especially
CC   cardiovascular diseases such as congestive heart failure caused by
CC   cardiac myocyte hypertrophy
XX
SQ   Sequence 1560 BP; 321 A; 449 C; 390 G; 400 T; 0 U; 0 Other;

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Qy        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
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Qy        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
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Qy        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
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Qy        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720
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Qy        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
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Qy       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
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Qy       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
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RESULT 2
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ID   ABQ81227 standard; cDNA; 1560 BP.
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AC   ABQ81227;
XX
DT   05-DEC-2002  (first entry)
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DE   Mouse 14273 nucleic acid, associated with metabolic disorder.
XX
KW   Mouse; 14273; metabolic disorder; obesity; diabetes; anorexia; cachexia;
KW   anorectic; antidiabetic; anabolic; transgenic animal; gene therapy; gene;
KW   ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             195. .1280
FT                   /*tag=  a
FT                   /product= "14273"
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PN   WO200267868-A2.
XX
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PD 06-SEP-2002.
XX
PF 26-FEB-2002; 2002WO-US006131.
XX
PR 26-FEB-2001; 2001US-0271655P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gimeno R, Tsai F;
XX
DR WPI; 2002-698629/75.
DR P-PSDB; ABB79907.
XX
PT Identifying a nucleic acid associated with a metabolic disorder, useful
PT for diagnosing metabolic disorders, e.g. obesity, comprises contacting
PT the sample with a probe comprising at least 25 contiguous nucleotides of
PT the 14273 gene.
XX
PS Claim 1; Fig 2; 95pp; English.
XX
CC The present sequence is that of a murine nucleic acid, designated 14273,
CC associated with metabolic disorders. 14273 molecules are expressed at
CC high levels in adipose tissue, e.g. white adipose tissue and brown
CC adipose tissue, as well as in pancreatic islets. They are upregulated
CC during exposure to cold (i.e. under conditions that affect brown or white
CC adipocyte metabolism) and downregulated in genetic models of obesity.
CC 14273 knock-out mice, when fed a high-fat diet, gain more weight and have
CC larger epididymal fat pads than wild-type mice. They also show increased
CC levels of glucose and insulin upon fasting. A 14273 agonist may be
CC beneficial to the treatment of obesity and/or type II diabetes by
CC preventing fat accumulation on a high-fat diet and/or the increases in
CC endogenous glucose production which occur in type II diabetes. The
CC present invention provides 14273 nucleic acids, polypeptides and
CC antibodies useful for the diagnosis and treatment of metabolic disorders
CC including obesity, anorexia, cachexia and diabetes. Also provided are
CC methods for identifying a subject having a metabolic disorder, for
CC identifying a compound capable of modulating metabolic activity, methods
CC for modulating metabolic activity or adipocyte activity (hyperplastic
CC growth, hypertrophic growth or lipogenesis), methods for modulating
CC lipogenesis or lipolysis in a subject, and a method for regulating
CC endogenous glucose levels
XX
SQ Sequence 1560 BP; 321 A; 449 C; 390 G; 400 T; 0 U; 0 Other;

Query Match 100.0%; Score 1560; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60

Qy         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120

Qy        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180

Qy        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240

Qy        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300

Qy        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360

Qy        361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420

Qy        421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480

Qy        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540

Qy        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600

Qy        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660

Qy        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720

Qy        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780

Qy        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840

Qy        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900

Qy        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960

Qy        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200

Qy       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260

Qy       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320

Qy       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380

Qy       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440

Qy       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500

Qy       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAAA 1560


RESULT 3
AAZ49746
ID   AAZ49746 standard; cDNA; 1561 BP.
XX
AC   AAZ49746;
XX
DT   02-MAY-2000  (first entry)
XX
DE   Murine 14273 G-protein coupled receptor (GPCR) encoding cDNA.
XX
KW   G-protein coupled receptor; GPCR; 14273 receptor; mouse; somatostatin;
KW   cellular function/activity; galanin receptor; chemokine receptor;
KW   diagnosis; treatment; receptor-mediated disorder; screening; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             195. .1280
FT                   /*tag=  a
FT                   /product= "Murine 14273 G-Protein coupled receptor"
FT                   /note= "Ortholog of human 14273 GPCR"
FT                   /transl_except= (pos:228. .230, aa:Gly)
FT                   /transl_except= (pos:315. .317, aa:Val)
FT                   /transl_except= (pos:1002. .1004, aa:Ile)
FT   unsure          987. .989
FT                   /*tag=  b
FT                   /note= "Encodes Thr"
XX
PN   WO200000611-A2.
XX
PD   06-JAN-2000.
XX
PF   30-JUN-1999;   99WO-US014842.
XX
PR   30-JUN-1998;   98US-00107761.
PR   30-DEC-1998;   98US-00223538.
PR   26-FEB-1999;   99US-00261599.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Glucksmann MA,  Tsai F;
XX
DR   WPI; 2000-147268/13.
DR   P-PSDB; AAY44663.
XX
PT   Novel G-protein coupled receptor 14273 polynucleotides and polypeptides
PT   used as a target for diagnosis and treatment of receptor-mediated
PT   disorders.
XX
PS   Claim 3a; Fig 7; 89pp; English.
XX
CC   The present sequence is the cDNA encoding mouse G-protein coupled
CC   receptor (GPCR) 14273 protein, an ortholog of human 14273 GPCR. It is
CC   involved in modulation of a cellular function or activity upon binding of
CC   a ligand to the GPCR. The GPCR 14273 protein has homology to galanin
CC   receptor, chemokine receptor and somatostatin. GPCR 14273 sequences are
CC   useful as a target for diagnosis and treatment of receptor-mediated
CC   disorders. The polypeptide is used for screening of drugs, agonist,
CC   antagonists and to produce antibodies. The antibodies are used for
CC   diagnosis, to assess abnormal tissue distribution or expression during
CC   development, inhibiting receptor function, tissue typing and forensic
CC   identification. The DNA sequences are used to detect genetic alterations
CC   in the gene and as a source of primers and probes
XX
SQ   Sequence 1561 BP; 321 A; 453 C; 386 G; 400 T; 0 U; 1 Other;

  Query Match           77.7%;  Score 1212;  DB 3;  Length 1561;
  Best Local Similarity  99.7%;  Pred. No. 0;
  Matches 1462;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60

Qy         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120

Qy        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180

Qy        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGCTCCCTCGCACA 240

Qy        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300

Qy        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTGGTGTTGAGCCTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360

Qy        361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420

Qy        421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480

Qy        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540

Qy        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600

Qy        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660

Qy        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720

Qy        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780

Qy        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840

Qy        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900

Qy        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960

Qy        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020
              |||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||
Db        961 CCCAACAAGACTACCGACTCTTCCGCASGCTCTTCCTGCTCATCGTTTCCTTCTTCATCA 1020

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200

Qy       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260

Qy       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320

Qy       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
                | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GCGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380

Qy       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440

Qy       1441 TCCTTAAAAGAACTTTCTATGGGTTCC 1467
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Db       1441 TCCTTAAAAGAACTTTCTATGGGTTCC 1467
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RESULT 4
AAA64344
ID AAA64344 standard; DNA; 180 BP.
XX
AC AAA64344;
XX
DT 20-DEC-2000 (first entry)
XX
DE Probe for murine G-protein coupled receptor designated cDNA.
XX
KW Human; G-protein coupled receptor; receptor-mediated disorder;
KW 14273 receptor; cardiovascular disease; congestive heart failure;
KW cardiac myocyte hypertrophy; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200050596-A2.
XX
PD 31-AUG-2000.
XX
PF 28-FEB-2000; 2000WO-US005068.
XX
PR 26-FEB-1999; 99US-00261599.
PR 08-DEC-1999; 99US-00456455.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Glucksmann MA, Tsai F;
XX
DR WPI; 2000-587184/55.
XX
PT 14273 receptor polynucleotides and polypeptides, useful in the diagnosis
PT and treatment of receptor-mediated disorders such as cardiovascular
PT diseases.
XX
PS Example 2; Page 77; 105pp; English.
XX
CC The present sequence represents a probe for cDNA encoding a murine G-
CC protein coupled receptor, designated 14273 receptor. The G-protein
CC coupled receptor 14273 polypeptide is used to produce antibodies, in drug
CC screening assays, and to screen for agonist and antagonists. The
CC antibodies are used for diagnostic applications, and to assess abnormal
CC tissue distributions or abnormal expression during development. The
CC antibodies are also useful for tissue typing, and in forensic
CC identification, as well as for inhibiting receptor function. The 14273
CC polynucleotides can be used to express the protein, to detect 14273 mRNA,
CC to detect genetic alterations in the 14273 gene, and as a source of
CC primers and probes. The 14273 polynucleotides and polypeptides are also
CC useful as a target for diagnosis and treatment of receptor-mediated
CC disorders, especially cardiovascular diseases such as congestive heart
CC failure caused by cardiac myocyte hypertrophy
XX
SQ Sequence 180 BP; 37 A; 54 C; 36 G; 53 T; 0 U; 0 Other;

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  Query Match             11.5%;  Score 180;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2e-63;
  Matches  180;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 60

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 120

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 180
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RESULT 5
AAA64345
ID AAA64345 standard; DNA; 138 BP.
XX
AC AAA64345;
XX
DT 20-DEC-2000 (first entry)
XX
DE Probe for murine G-protein coupled receptor designated cDNA.
XX
KW Human; G-protein coupled receptor; receptor-mediated disorder;
KW 14273 receptor; cardiovascular disease; congestive heart failure;
KW cardiac myocyte hypertrophy; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200050596-A2.
XX
PD 31-AUG-2000.
XX
PF 28-FEB-2000; 2000WO-US005068.
XX
PR 26-FEB-1999; 99US-00261599.
PR 08-DEC-1999; 99US-00456455.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Glucksmann MA, Tsai F;
XX
DR WPI; 2000-587184/55.
XX
PT 14273 receptor polynucleotides and polypeptides, useful in the diagnosis
PT and treatment of receptor-mediated disorders such as cardiovascular
PT diseases.
XX
PS Example 2; Page 77; 105pp; English.
XX
CC The present sequence represents a probe for cDNA encoding a murine G-
CC protein coupled receptor, designated 14273 receptor. The G-protein
CC coupled receptor 14273 polypeptide is used to produce antibodies, in drug
CC screening assays, and to screen for agonist and antagonists. The
CC antibodies are used for diagnostic applications, and to assess abnormal
CC tissue distributions or abnormal expression during development. The

```
CC   antibodies are also useful for tissue typing, and in forensic
CC   identification, as well as for inhibiting receptor function. The 14273
CC   polynucleotides can be used to express the protein, to detect 14273 mRNA,
CC   to detect genetic alterations in the 14273 gene, and as a source of
CC   primers and probes. The 14273 polynucleotides and polypeptides are also
CC   useful as a target for diagnosis and treatment of receptor-mediated
CC   disorders, especially cardiovascular diseases such as congestive heart
CC   failure caused by cardiac myocyte hypertrophy
XX
SQ   Sequence 138 BP; 30 A; 46 C; 26 G; 36 T; 0 U; 0 Other;

  Query Match             8.8%;  Score 138;  DB 3;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-46;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        909 AAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAA 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAA 60

Qy        969 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 120

Qy       1029 CCCATCATCATCACCATC 1046
              ||||||||||||||||||
Db        121 CCCATCATCATCACCATC 138


RESULT 6
ABT04869
ID   ABT04869 standard; cDNA; 1086 BP.
XX
AC   ABT04869;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Human G protein coupled receptor hRUP31 coding sequence.
XX
KW   Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
KW   hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200242461-A2.
XX
PD   30-MAY-2002.
XX
PF   26-NOV-2001; 2001WO-US044386.
XX
PR   27-NOV-2000; 2000US-0253404P.
PR   12-DEC-2000; 2000US-0255366P.
PR   20-FEB-2001; 2001US-0270266P.
PR   20-FEB-2001; 2001US-0270286P.
PR   06-APR-2001; 2001US-0282032P.
PR   06-APR-2001; 2001US-0282356P.
PR   06-APR-2001; 2001US-0282358P.
PR   06-APR-2001; 2001US-0282365P.
PR   14-MAY-2001; 2001US-0290917P.
PR   31-JUL-2001; 2001US-0309208P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Chen R,  Chu ZL,  Dang HT,  Lowitz KP,  Pride C;
XX
DR   WPI; 2002-566565/60.
DR   P-PSDB; ABJ04071.
XX
PT   Novel endogenous and non-endogenous versions of G protein-coupled
PT   receptor useful for identification of candidate compounds as receptor
PT   agonists or antagonists for use as therapeutic agents.
XX
PS   Claim 15; Page 61; 84pp; English.
XX
CC   The present invention provides the protein and coding sequences of
CC   several human G-protein coupled receptors (GPCRs). These can be used in
CC   the identification of candidate compounds as receptor agonists or inverse
CC   agonists having applicability as therapeutic agents. The present sequence
CC   is a GPCR coding sequence of the invention
XX
SQ   Sequence 1086 BP; 185 A; 346 C; 295 G; 260 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 44;  DB 6;  Length 1086;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 701


RESULT 7
ABS73398
ID   ABS73398 standard; DNA; 1086 BP.
XX
AC   ABS73398;
XX
DT   04-DEC-2002  (first entry)
XX
DE   DNA encoding human GPCR HF1948 mutant I128F.
XX
KW   Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
KW   hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
KW   psychotic disorder; asthma; bronchospasm; anaesthesia;
KW   myocardial infarction; MI; stroke; glaucoma; anxiety;
KW   prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
KW   prostatic hypertrophy; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200268600-A2.
XX
PD   06-SEP-2002.
XX
PF   26-FEB-2002; 2002WO-US005625.
XX
PR   26-FEB-2001; 2001US-0271913P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Liaw CW,  Chalmers DT,  Behan DP,  Maciejewski-Lenior D,  Leonard JN;
PI   Lin I,  Ortuno D;
XX
DR   WPI; 2002-706980/76.
DR   P-PSDB; ABG95169.
XX
PT   New human G-protein coupled receptor (GPCR), useful for screening agonist
PT   or inverse agonist compounds for treating diseases associated with GPCR.
XX
PS   Example 2; Page 180-181; 201pp; English.
XX
CC   The present invention relates to transmembrane receptors, particularly
CC   endogenous human G-protein coupled receptors (GPCRs), mutant (non-
CC   endogenous) versions of the GPCRs, and the polynucleotide sequences
CC   encoding them. The GPCRs are useful for screening agonist or inverse
CC   agonist compounds for treating diseases associated with GPCR. Diseases
CC   that can be treated with such compounds include allergies, hypertension,
CC   reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
CC   disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),
CC   stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
CC   anxiety, prostatic hypertrophy, rhinitis, and angina. The present
CC   sequence encodes a mutant human GPCR
XX
SQ   Sequence 1086 BP; 181 A; 348 C; 295 G; 262 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 44;  DB 6;  Length 1086;
```

```
  Best Local Similarity   100.0%;  Pred. No. 4.6e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 701


RESULT 8
ABS73399
ID   ABS73399 standard; DNA; 1086 BP.
XX
AC   ABS73399;
XX
DT   04-DEC-2002  (first entry)
XX
DE   DNA encoding human GPCR HF1948 mutant E135N.
XX
KW   Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
KW   hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
KW   psychotic disorder; asthma; bronchospasm; anaesthesia;
KW   myocardial infarction; MI; stroke; glaucoma; anxiety;
KW   prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
KW   prostatic hypertrophy; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200268600-A2.
XX
PD   06-SEP-2002.
XX
PF   26-FEB-2002; 2002WO-US005625.
XX
PR   26-FEB-2001; 2001US-0271913P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Liaw CW,  Chalmers DT,  Behan DP,  Maciejewski-Lenior D,  Leonard JN;
PI   Lin I,  Ortuno D;
XX
DR   WPI; 2002-706980/76.
DR   P-PSDB; ABG95170.
XX
PT   New human G-protein coupled receptor (GPCR), useful for screening agonist
PT   or inverse agonist compounds for treating diseases associated with GPCR.
XX
PS   Example 2; Page 183; 201pp; English.
XX
CC   The present invention relates to transmembrane receptors, particularly
CC   endogenous human G-protein coupled receptors (GPCRs), mutant (non-
CC   endogenous) versions of the GPCRs, and the polynucleotide sequences
CC   encoding them. The GPCRs are useful for screening agonist or inverse
CC   agonist compounds for treating diseases associated with GPCR. Diseases
CC   that can be treated with such compounds include allergies, hypertension,
CC   reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
CC   disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),
CC   stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
CC   anxiety, prostatic hypertrophy, rhinitis, and angina. The present
CC   sequence encodes a mutant human GPCR
XX
SQ   Sequence 1086 BP; 183 A; 348 C; 293 G; 262 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 44;  DB 6;  Length 1086;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 701


RESULT 9
ABS73343
ID   ABS73343 standard; cDNA; 1086 BP.
XX
AC   ABS73343;
XX
DT   04-DEC-2002  (first entry)
XX
DE   cDNA encoding human GPCR HF1948.
XX
KW   Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
KW   hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
KW   psychotic disorder; asthma; bronchospasm; anaesthesia;
KW   myocardial infarction; MI; stroke; glaucoma; anxiety;
KW   prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
KW   prostatic hypertrophy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200268600-A2.
XX
PD   06-SEP-2002.
XX
PF   26-FEB-2002; 2002WO-US005625.
XX
PR   26-FEB-2001; 2001US-0271913P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Liaw CW,  Chalmers DT,  Behan DP,  Maciejewski-Lenior D,  Leonard JN;
PI   Lin I,  Ortuno D;
XX
DR   WPI; 2002-706980/76.
DR   P-PSDB; ABG95157.
XX
PT   New human G-protein coupled receptor (GPCR), useful for screening agonist
PT   or inverse agonist compounds for treating diseases associated with GPCR.
XX
PS   Claim 23; Page 122-123; 201pp; English.
XX
CC   The present invention relates to transmembrane receptors, particularly
CC   endogenous human G-protein coupled receptors (GPCRs), mutant (non-
CC   endogenous) versions of the GPCRs, and the polynucleotide sequences
CC   encoding them. The GPCRs are useful for screening agonist or inverse
CC   agonist compounds for treating diseases associated with GPCR. Diseases
CC   that can be treated with such compounds include allergies, hypertension,
CC   reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
CC   disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),
CC   stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
CC   anxiety, prostatic hypertrophy, rhinitis, and angina. The present
CC   sequence encodes an endogenous human GPCR
XX
SQ   Sequence 1086 BP; 182 A; 348 C; 295 G; 261 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 44;  DB 6;  Length 1086;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 701


RESULT 10
ACA60998
ID   ACA60998 standard; cDNA; 1086 BP.
XX
AC   ACA60998;
XX
DT   04-JUL-2003  (first entry)
XX
DE   cDNA encoding novel human G protein coupled receptor HGPRBMY18.
XX
KW   Human; G protein coupled receptor; GPCR; HGPRBMY18; cytostatic;
```

```
KW   nootropic; neuroprotective; antiparkinsonian; antidiabetic;
KW   antidepressant; hypotensive; tranquilizer; nephrotropic;
KW   cell growth disorder; neurological condition; pituitary gland disorder;
KW   colon disorder; breast disorder; lung disorder; prostate disorder;
KW   Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
KW   colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
KW   sleeplessness; hypertension; anxiety; stress; renal failure; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1083
FT                   /*tag= a
FT                   /product= "HGPRBMY18"
FT                   /note= "Human G protein coupled receptor"
XX
PN   US2003022186-A1.
XX
PD   30-JAN-2003.
XX
PF   14-NOV-2001; 2001US-00992331.
XX
PR   14-NOV-2000; 2000US-0248483P.
PR   16-JAN-2001; 2001US-0261782P.
PR   27-JUL-2001; 2001US-0308540P.
XX
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
XX
PI   Feder JN,  Mintier G,  Ramanathan CS;
XX
DR   WPI; 2003-416985/39.
DR   P-PSDB; ABU09715.
XX
PT   New isolated human GPCR, HGPRBMYB18, polynucleotide and polypeptide,
PT   useful for treating, diagnosing and preventing disorders such as cancer,
PT   neurological conditions, and diseases of the pituitary gland, colon,
PT   breast and lungs.
XX
PS   Claim 1; Fig 1; 66pp; English.
XX
CC   The invention describes a new isolated polynucleotide encoding a human G-
CC   protein coupled receptor (GPCR) or its functional fragment. The methods
CC   and compositions of the present invention are useful for treating,
CC   diagnosing, preventing and screening disorders associated with aberrant
CC   cell growth, neurological conditions, and diseases related to the
CC   pituitary gland, colon, breast, lungs and prostate. These disorders
CC   include Alzheimer's, Parkinson, diabetes, dwarfism, colour blindness,
CC   retinal pigmentosa, asthma, depression, schizophrenia, sleeplessness,
CC   hypertension, anxiety, stress and renal failure. This sequence encodes
CC   novel human G protein coupled receptor HGPRBMY18
XX
SQ   Sequence 1086 BP; 182 A; 349 C; 295 G; 260 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 44;  DB 7;  Length 1086;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 701


RESULT 11
ADB47641
ID   ADB47641 standard; cDNA; 1086 BP.
XX
AC   ADB47641;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human cDNA encoding GPCR, HGPRBMY18.
XX
KW   Human; ss; gene; G protein-coupled receptor; GPCR; endocrine disorder;
KW   pituitary disorder; growth hormone; prolactin; luteinising hormone;
KW   follicle-stimulating hormone; thyroid-stimulating hormone;
KW   adrenocorticotropin; vasopressin; oxytocin; aberrant growth;
KW   aberrant lactation; aberrant sexual characteristic development;
KW   testosterone; oestrogen; aberrant water homeostasis; hypogonadism;
KW   Addison's disease; hypothyroidism; Cushing's disease; agromegaly;
KW   gigantism; lethargy; osteoporosis; aberrant calcium homeostasis;
KW   aberrant potassium homeostasis; reproductive disorder;
KW   developmental disorder; colon cancer; breast cancer; prostate cancer;
KW   lung cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1086
FT                   /*tag= b
FT                   /product= "HGPRBMY18"
FT                   /transl_except= (pos:364. .372,aa:Gly-Val)
FT   misc_feature    1. .1083
FT                   /*tag= a
FT                   /note= "Claimed in claim 1"
FT   misc_feature    4. .1083
FT                   /*tag= c
FT                   /note= "Claimed in claim 1"
XX
PN   US2003129653-A1.
XX
PD   10-JUL-2003.
XX
PF   30-SEP-2002; 2002US-00262313.
XX
PR   16-JAN-2001; 2001US-0261782P.
PR   27-JUL-2001; 2001US-0308540P.
PR   14-NOV-2001; 2001US-00992331.
XX
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
XX
PI   Feder JN,  Mintier G,  Ramanathan CS,  Hawken DR;
XX
DR   WPI; 2003-678603/64.
DR   P-PSDB; ADB47642.
XX
PT   New human G-protein coupled receptor, HGPRBMY18, useful for treating and
PT   diagnosing disease such as cancer, hypothyroidism, Cushing's disease and
PT   osteoporosis.
XX
PS   Claim 1; Fig 1; 71pp; English.
XX
CC   The invention relate to an isolated human G protein-coupled receptor
CC   (GPCR), HGPRBMY18, polynucleotide encoding a novel human GPCR HGPRBMY18.
CC   Also included are expression vectors, host cells, a fusion protein
CC   comprising HGPRBMY18 and an Fc portion of a human immunoglobulin protein,
CC   an anti-HGPRBMY18 antibody its antigenic epitope, screening a library of
CC   molecules or compounds with a polynucleotide to identify at least one
CC   molecule or compound which specifically binds to the polynucleotide
CC   sequence and screening for candidate compounds capable of modulating
CC   activity of a G-protein coupled receptor-encoding polypeptide. HGPRBMY18
CC   or its (ant)agonist (small molecule, peptide, and antisense molecule) is
CC   useful for treating a disease, disorder, or condition related to the
CC   endocrine, gastrointestinal, reproductive, pulmonary, or neural system.
CC   Diseases include endocrine disorders, disorders of the pituitary,
CC   aberrant growth hormone synthesis and/or secretion, aberrant prolactin
CC   synthesis and/or secretion, aberrant luteinising hormone synthesis and/or
CC   secretion, aberrant follicle-stimulating hormone synthesis and/or
CC   secretion, aberrant thyroid-stimulating hormone synthesis and/or
CC   secretion, aberrant adrenocorticotropin synthesis and/or secretion,
CC   aberrant vasopressin secretion, aberrant oxytocin secretion, aberrant
CC   growth, aberrant lactation, aberrant sexual characteristic development,
```

```
CC   aberrant testosterone synthesis and/or secretion, aberrant oestrogen
CC   synthesis and/or secretion, aberrant water homeostasis, hypogonadism,
CC   Addison's disease, hypothyroidism, Cushing's disease, agromegaly,
CC   gigantism, lethargy, osteoporosis, aberrant calcium homeostasis, aberrant
CC   potassium homeostasis, reproductive disorders, developmental disorders,
CC   colon cancer, related proliferative condition of the colon, breast
CC   cancer, related proliferative condition of the breast, prostate cancer,
CC   related proliferative condition of the prostate, lung cancer, and related
CC   proliferative condition of the lung. In addition determining the presence
CC   or amount of expression of HGPRBMY18 is useful for diagnosing a
CC   (susceptibility to a) pathological condition such as colon cancer,
CC   related proliferative condition of the colon, breast cancer, related
CC   proliferative condition of the breast, prostate cancer, related
CC   proliferative condition of the prostate, lung cancer, and related
CC   proliferative condition of the lung. The present sequence encodes
CC   HGPRBMY18.
XX
SQ   Sequence 1086 BP; 182 A; 349 C; 295 G; 260 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 44;  DB 8;  Length 1086;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 701


RESULT 12
ABX10627
ID   ABX10627 standard; DNA; 1160 BP.
XX
AC   ABX10627;
XX
DT   11-APR-2003  (first entry)
XX
DE   DNA encoding human orphan SNORF49 receptor.
XX
KW   Human; gene; ds; SNORF49 receptor; neuroregulator; inflammation;
KW   arthritis; autoimmune disease; transplant rejection; infection;
KW   septicaemia; AIDS; neurological disorder; schizophrenia; epilepsy;
KW   respiratory disorder; asthma; obesity; diabetes; anorexia;
KW   cardiovascular disorder; ischaemia; stroke; cancer; sexual disorder;
KW   reproductive disorder; circadian rhythm disorder; renal disorder;
KW   bone disease; osteoporosis; allergy; Parkinson's disease;
KW   Alzheimer's disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             28. .1113
FT                   /*tag= a
FT                   /product= "SNORF49 receptor"
XX
PN   US2002151705-A1.
XX
PD   17-OCT-2002.
XX
PF   11-DEC-2001; 2001US-00015498.
XX
PR   05-OCT-1999;   99US-00412933.
XX
PA   (SMIT/) SMITH K E.
PA   (QUAN/) QUAN Y.
XX
PI   Smith KE,  Quan Y;
XX
DR   WPI; 2003-198336/19.
DR   P-PSDB; ABG73199.
XX
PT   New recombinant nucleic acid comprising a nucleic acid encoding a
PT   mammalian SNORF49 receptor, useful for screening antagonist to the
PT   SNORF49 receptor or as probes to obtain homologous nucleic acids from
PT   other species.
XX
PS   Claim 2; Fig 1; 13pp; English.
XX
CC   The invention discloses a recombinant nucleic acid comprising a nucleic
CC   acid encoding a mammalian SNORF49 receptor, having a sequence identical
CC   to the sequence of the human SNORF49 receptor-encoding nucleic acid
CC   contained in plasmid pEXJ.T73BS-hS-NORF49-f. SNORF49 receptor is a
CC   neuroregulator. The nucleic acid is useful for expressing the receptor in
CC   transfected cells, for screening for antagonists to the SNORF49 receptor
CC   or as probes to obtain homologous nucleic acids from other species and to
CC   detect the existence of nucleic acids having complementary sequences in
CC   samples. The receptor can also be used in the design of drugs for
CC   treating various pathophysiological conditions, such as inflammation,
CC   arthritis, autoimmune disease, transplant rejection, infections,
CC   septicaemia, AIDS, neurological disorders, such as schizophrenia and
CC   epilepsy, respiratory disorders, asthma, obesity, diabetes, anorexia,
CC   cardiovascular disorders, ischaemia, stroke, cancer, sexual/reproductive
CC   disorders, circadian rhythm disorders, renal disorders, bone diseases,
CC   osteoporosis, allergy, Parkinson's disease and Alzheimer's disease. The
CC   sequence presented is the DNA encoding the human orphan SNORF49 receptor
XX
SQ   Sequence 1160 BP; 192 A; 372 C; 318 G; 278 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 44;  DB 7;  Length 1160;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        685 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 728


RESULT 13
AAD08854
ID   AAD08854 standard; cDNA; 1321 BP.
XX
AC   AAD08854;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human G-protein coupled receptor-20 (GCREC-20) cDNA.
XX
KW   Human; G-protein coupled receptor-20; GCREC-20; gene therapy; cirrhosis;
KW   transgenic animal; proliferative disorder; actinic keratosis;
KW   hepatitis nephrotropic; cancer; breast; bladder; bone marrow; brain;
KW   uterus; leukaemia; adenocarcinoma; lymphoma; melanoma; myeloma; epilepsy;
KW   stroke; neurological disorder; Alzheimer's disease; Parkinson's disease;
KW   nausea; Huntington's disease; multiple sclerosis; dementia;
KW   angina pectoris; central nervous system disorder;
KW   cardiovascular disorder; hypertension; atherosclerosis;
KW   congestive heart failure; gastrointestinal disorder; dysphagia;
KW   peptic oesophagitis; spasm; gastritis; anorexia; pyrosis; pancreatitis;
KW   Crohn's disease; diarrhoea; autoimmune disorder; anaemia;
KW   inflammatory disorder; Acquired Immune Deficiency Syndrome; AIDS;
KW   Addison's diseases; allergy; asthma; diabetes mellitus; antithyroid;
KW   atopic dermatitis; glomerulonephritis; Grave's disease; psoriasis;
KW   rheumatoid arthritis; ulcerative colitis; osteoporosis; antifungal;
KW   metabolic disorder; obesity; nootropic; protozoacide; virucide; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             30. .1115
FT                   /*tag= a
FT                   /product= "Human GCREC-20 protein"
XX
PN   WO200142288-A2.
XX
PD   14-JUN-2001.
XX
PF   07-DEC-2000; 2000WO-US033382.
XX
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PR   10-DEC-1999;   99US-0172852P.
PR   22-DEC-1999;   99US-0171732P.
PR   14-JAN-2000; 2000US-0176148P.
PR   21-JAN-2000; 2000US-0177331P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Burford N,  Baughn MR,  Au-Young J,  Yang J,  Lu DAM,  Reddy R;
XX
DR   WPI; 2001-381635/40.
DR   P-PSDB; AAE04564.
XX
PT   New human G-protein coupled receptor polypeptides for diagnosing,
PT   preventing, and treating cell proliferative, neurological,
PT   cardiovascular, gastrointestinal, autoimmune and metabolic disorders.
XX
PS   Claim 5; Page 167; 175pp; English.
XX
CC   The present sequence is human G-protein coupled receptor-20 (GCREC-20)
CC   cDNA. GCREC is useful in somatic or germline gene therapy to correct a
CC   genetic deficiency, to express a conditionally lethal gene product and to
CC   express a protein which affords protection against intracellular
CC   parasites and also for diagnosis of disorders associated with expression
CC   of GCREC. GCREC is also useful for generating hybridisation probes useful
CC   in mapping the naturally occurring genomic sequences and to create
CC   knockin humanised animals (pigs) or transgenic animals (mice or rats) to
CC   model human diseases. GCREC is used to diagnose, prevent and treat
CC   proliferative disorders (actinic keratosis, arteriosclerosis, cirrhosis,
CC   hepatitis and cancer); cancer (breast, bladder, bone marrow, brain,
CC   uterus cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma)
CC   neurological disorders (epilepsy, stroke, Alzheimer's, Huntington's,
CC   Parkinson's disease, multiple sclerosis, dementia and other central
CC   nervous system disorders); cardiovascular disorders (angina pectoris,
CC   hypertension, atherosclerosis, congestive heart failure);
CC   gastrointestinal disorders (dysphagia, peptic oesophagitis, oesophageal
CC   spasm, gastritis, gastric carcinoma, anorexia, nausea, abdominal angina,
CC   pyrosis, pancreatitis, Crohn's disease, diarrhoea); autoimmune/
CC   inflammatory disorders (acquired immunodeficiency syndrome (AIDS),
CC   Addison's diseases, allergies, anaemia, asthma, diabetes mellitus, atopic
CC   dermatitis, glomerulonephritis, Grave's disease, osteoarthritis,
CC   psoriasis, rheumatoid arthritis, ulcerative colitis, bacterial, fungal,
CC   parasitic, protozoal and helminthic infections) and metabolic disorders
CC   (obesity, osteoporosis, viral infections)
XX
SQ   Sequence 1321 BP; 243 A; 404 C; 348 G; 326 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 44;  DB 4;  Length 1321;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        687 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 730


RESULT 14
AAI66039
ID   AAI66039 standard; cDNA; 1458 BP.
XX
AC   AAI66039;
XX
DT   08-JAN-2002  (first entry)
XX
DE   Human G protein-coupled receptor encoding cDNA SEQ ID NO 2.
XX
KW   Human; G protein-coupled receptor; cytostatic; cancer; hypohypophysism;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             58. .1143
FT                   /*tag=  a
FT                   /product= "G protein-coupled receptor"
FT                   /note= "claimed in claim 6"
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PN   JP2001211885-A.
XX
PD   07-AUG-2001.
XX
PF   02-FEB-2000; 2000JP-00024921.
XX
PR   02-FEB-2000; 2000JP-00024921.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
DR   WPI; 2001-629567/73.
DR   P-PSDB; AAM51426.
XX
PT   A new G protein-coupled receptor polypeptide.
XX
PS   Claim 6; Page 41-42; 52pp; Japanese.
XX
CC   The invention relates to a human G protein-coupled receptor polypeptide
CC   with cytostatic activity and used for the treatment of cancers or
CC   hypohypophysism
XX
SQ   Sequence 1458 BP; 271 A; 445 C; 386 G; 356 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 44;  DB 4;  Length 1458;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-08;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        715 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 758


RESULT 15
ABZ42599
ID   ABZ42599 standard; DNA; 1737 BP.
XX
AC   ABZ42599;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human G protein-coupled receptor 14273 nucleotide SEQ ID NO:681.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
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OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC,  Roush CL,  Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   P-PSDB; ABP81754.
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XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 1737 BP; 377 A; 487 C; 440 G; 430 T; 0 U; 3 Other;

Query Match 2.8%; Score 44; DB 7; Length 1737;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: September 30, 2004, 22:12:48
Job time : 572.119 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 21:52:37 ; Search time 731.589 Seconds
(without alignments)
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Title: US-10-077-698-5
Perfect score: 1560
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3340653 seqs, 2534783454 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1560	100.0	1560	15	US-10-077-698-5	Sequence 5, Appli
3	1560	100.0	1560	15	US-10-171-027-5	Sequence 5, Appli
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5	1086	69.6	1086	14	US-10-086-181-6	Sequence 6, Appli
6	181	11.6	181	15	US-10-171-027-14	Sequence 14, Appl
7	138	8.8	138	15	US-10-171-027-15	Sequence 15, Appl
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18	44	2.8	1086	15	US-10-083-168-11	Sequence 11, Appl
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33	40	2.6	3173	15	US-10-116-252-5	Sequence 5, Appli
34	39	2.5	638	9	US-09-828-644-58	Sequence 58, Appl
c 35	38	2.4	203	10	US-09-535-459-1916	Sequence 1916, Ap
c 36	38	2.4	217	10	US-09-535-459-1915	Sequence 1915, Ap
c 37	38	2.4	221	10	US-09-535-459-1919	Sequence 1919, Ap
38	38	2.4	241	9	US-09-879-536-472	Sequence 472, App
c 39	38	2.4	250	10	US-09-535-459-1923	Sequence 1923, Ap
c 40	38	2.4	254	10	US-09-535-459-1921	Sequence 1921, Ap
c 41	38	2.4	273	10	US-09-535-459-1926	Sequence 1926, Ap
c 42	38	2.4	278	10	US-09-535-459-1913	Sequence 1913, Ap
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c 45	38	2.4	283	10	US-09-535-459-1925	Sequence 1925, Ap

ALIGNMENTS

RESULT 1
US-10-086-181-4
; Sequence 4, Application US/10086181
; Publication No. US20020177151A1
; GENERAL INFORMATION:
; APPLICANT: GIMENO, Ruth
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; TITLE OF INVENTION: DISORDERS, INCLUDING OBESITY AND DIABETES
; FILE REFERENCE: MNI-220
; CURRENT APPLICATION NUMBER: US/10/086,181
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/271,655
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Murine ortholog
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (195)...(1280)
US-10-086-181-4

Query Match 100.0%; Score 1560; DB 14; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 5, Application US/10077698
; Publication No. US20030008350A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 14273 Receptor, A No. US20030008350A1el G-Protein Coupled Receptor
; FILE REFERENCE: 5800-4B, 035800/177086
; CURRENT APPLICATION NUMBER: US/10/077,698
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/261,599
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/107,761
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
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; ORGANISM: Murine ortholog
US-10-077-698-5

Query Match 100.0%; Score 1560; DB 15; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
Db       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
Qy       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
Db       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
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RESULT 3
US-10-171-027-5
; Sequence 5, Application US/10171027
; Publication No. US20030073168A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: 14273 Receptor, A No. US20030073168A1el G-Protein Coupled Recepto
; FILE REFERENCE: MNI-204CP3
; CURRENT APPLICATION NUMBER: US/10/171,027
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/456,455
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 09/223,538
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Murine ortholog
US-10-171-027-5

Query Match 100.0%; Score 1560; DB 15; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60
Db          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60
Qy         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
Db         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
Qy        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
Db        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
Qy        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
Db        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
Qy        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
Db        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
Qy        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
Db        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
Qy        361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
Db        361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
Qy        421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
Db        421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
Qy        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
Db        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
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Qy        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600
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Db        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600

Qy        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660

Qy        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720

Qy        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780

Qy        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840

Qy        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900

Qy        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960

Qy        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
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Db       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200

Qy       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260

Qy       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320

Qy       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380

Qy       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440

Qy       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500

Qy       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
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RESULT 4
US-10-075-987-5
; Sequence 5, Application US/10075987
; Publication No. US20030166061A1

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; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  TITLE OF INVENTION: 14273 Receptor, A No. US20030166061A1el G-Protein Coupled Recepto
;  FILE REFERENCE: 5800-4B, 035800/177086
;  CURRENT APPLICATION NUMBER: US/10/075,987
;  CURRENT FILING DATE:  2002-02-13
;  PRIOR APPLICATION NUMBER: US/09/261,599B
;  PRIOR FILING DATE: 1999-02-26
;  PRIOR APPLICATION NUMBER: 09/223,538
;  PRIOR FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1560
;   TYPE: DNA
;   ORGANISM: Murine ortholog
US-10-075-987-5

  Query Match            100.0%;  Score 1560;  DB 15;  Length 1560;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1560;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60
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Db          1 TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGC 60

Qy         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCACACCATCAGTGACCACTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGCGGAG 120

Qy        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTCCCGGACGCGTGG 180

Qy        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCGGGCGCCCGGCATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACA 240

Qy        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTGGACCAAGTCAATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACC 300

Qy        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTGGTGTTGAGCGTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGC 360

Qy        361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGCAACGTGTGTGCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCA 420

Qy        421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCTGGTGCTCAACCTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGC 480

Qy        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCGTCGTGCGCTGGACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCT 540

Qy        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGTGATGACAATGAGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGC 600

Qy        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCATGGTGTGCATCGTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGG 660

Qy        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCACTGCTGGCTTTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCT 720

Qy        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGTTCCGCGTGGTCCCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACAT 780
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Qy        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGATTGGCCCAACCGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACT 840

Qy        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTGGTGCCGGGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAG 900

Qy        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CATCGCGGAAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGT 960

Qy        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCCAACAAGACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCA 1020

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200

Qy       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTTCTTTTTTCCAGAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACT 1260

Qy       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTCTGTTATTTCCAGCTAACTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAA 1320

Qy       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGGAGTTAACTTCAAGGAAAGCCCACCAGTGCGCCCTGCTTTAAAAATACCCGACTTCCA 1380

Qy       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACAGCAGGCATCTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATTTT 1440

Qy       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TCCTTAAAAGAACTTTCTATGGGTTCCTTTTGTGAACTTTTTTAAGTGTGTTTGTAATAT 1500

Qy       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATCTAGTTAATAAATTTTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAAAA 1560
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RESULT 5
US-10-086-181-6
; Sequence 6, Application US/10086181
; Publication No. US20020177151A1
; GENERAL INFORMATION:
;  APPLICANT: GIMENO, Ruth
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
;  TITLE OF INVENTION:  DISORDERS, INCLUDING OBESITY AND DIABETES
;  FILE REFERENCE: MNI-220
;  CURRENT APPLICATION NUMBER: US/10/086,181
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: 60/271,655
;  PRIOR FILING DATE: 2001-02-26
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Murine ortholog
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US-10-086-181-6

Query Match 69.6%; Score 1086; DB 14; Length 1086;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        195 ATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACACCCTGGACCAAGTC 254
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Db          1 ATGTCCCCTGAGTGTGCACAGACGACGGGCCCTGGTCCCTCGCACACCCTGGACCAAGTC 60

Qy        255 AATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACCGGTTGGTGTTGAGC 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCGCACCCACTTCCCTTTCTTCTCGGATGTCAAGGGCGACCACCGGTTGGTGTTGAGC 120

Qy        315 GTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGCTGGGCAACGTGTGT 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCGTGGAGACCACCGTTCTGGGACTCATCTTTGTCGTCTCACTGCTGGGCAACGTGTGT 180

Qy        375 GCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCAGCCTGGTGCTCAAC 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTCTAGTGCTGGTGGCGCGCCGTCGGCGCCGTGGGGCGTCAGCCAGCCTGGTGCTCAAC 240

Qy        435 CTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGCTCGTCGTGCGCTGG 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTTCTGCGCGGATTTGCTCTTCACCAGCGCCATCCCTCTAGTGCTCGTCGTGCGCTGG 300

Qy        495 ACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCTACGTGATGACAATG 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGAGGCCTGGCTGTTGGGGCCCGTCGTCTGCCACCTGCTCTTCTACGTGATGACAATG 360

Qy        555 AGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGCGGCAGCGTCACGATCCTCACACTGGCCGCGGTCAGCCTGGAGCGCATGGTGTGCATC 420

Qy        615 GTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGGCGGCACTGCTGGCT 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCGCCTCCGGCGCGGCTTGAGCGGCCCGGGGCGGCGGACTCAGGCGGCACTGCTGGCT 480

Qy        675 TTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCTTGTTCCGCGTGGTC 734
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Db        481 TTCATATGGGGTTACTCGGCGCTCGCCGCGCTGCCCCTCTACATCTTGTTCCGCGTGGTC 540

Qy        735 CCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACATTGGATTGGCCCAAC 794
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Db        541 CCGCAGCGCCTTCCCGGCGGGGACCAGGAAATTCCGATTTGCACATTGGATTGGCCCAAC 600

Qy        795 CGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACTTCCTGGTGCCGGGA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGCATAGGAGAAATCTCATGGGATGTGTTTTTTGAGACTTTGAACTTCCTGGTGCCGGGA 660

Qy        855 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAGCATCGCGGAAGAGG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCACGAAAGCATCGCGGAAGAGG 720

Qy        915 CTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAAGACTAC 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAAGACTAC 780

Qy        975 CGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCATC 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGTCCCATC 840

Qy       1035 ATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGGTCATCTGGCCA 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 ATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACCTGGTCATCTGGCCA 900

Qy       1095 TCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCTAAACCCCATACTG 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCCTAAACCCCATACTG 960

Qy       1155 TACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTGCTTCTTTTTTCCA 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 TACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCTGCTTCTTTTTTCCA 1020
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Qy       1215 GAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACTTGTCTGTTATTTCC 1274
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Db       1021 GAGAAGGGAGCCATTTTTACAGATACGTCTGTCAGGCGAAATGACTTGTCTGTTATTTCC 1080

Qy       1275 AGCTAA 1280
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Db       1081 AGCTAA 1086


RESULT 6
US-10-171-027-14
; Sequence 14, Application US/10171027
; Publication No. US20030073168A1
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: 14273 Receptor, A No. US20030073168A1el G-Protein Coupled Receptc
;  FILE REFERENCE: MNI-204CP3
;  CURRENT APPLICATION NUMBER: US/10/171,027
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US/09/456,455
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: 09/223,538
;  PRIOR FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 181
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-171-027-14

  Query Match             11.6%;  Score 181;  DB 15;  Length 181;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-82;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1021 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGTGGAGTCCCATCATCATCACCATCCTCCTCATCTTGATCCAAAACTTCCGGCAGGACC 60

Qy       1081 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGTCATCTGGCCATCCCTTTTCTTCTGGGTGGTGGCCTTCACGTTTGCCAACTCTGCCC 120

Qy       1141 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAAACCCCATACTGTACAACATGTCGCTGTTCAGGAACGAATGGAGGAAGATTTTTTGCT 180

Qy       1201 G 1201
             |
Db        181 G 181


RESULT 7
US-10-171-027-15
; Sequence 15, Application US/10171027
; Publication No. US20030073168A1
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: 14273 Receptor, A No. US20030073168A1el G-Protein Coupled Receptc
;  FILE REFERENCE: MNI-204CP3
;  CURRENT APPLICATION NUMBER: US/10/171,027
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US/09/456,455
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: 09/223,538
;  PRIOR FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 138
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-171-027-15

  Query Match              8.8%;  Score 138;  DB 15;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-60;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        909 AAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAA 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGAGGCTTACGCTGAGCTTGGCATACTCTGAGAGCCACCAGATCCGAGTGTCCCAACAA 60

Qy        969 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTACCGACTCTTCCGCACGCTCTTCCTGCTCATGGTTTCCTTCTTCATCATGTGGAGT 120

Qy       1029 CCCATCATCATCACCATC 1046
              ||||||||||||||||||
Db        121 CCCATCATCATCACCATC 138


RESULT 8
US-09-535-459-1891/c
; Sequence 1891, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULES
;  FILE REFERENCE: PD-1014 CIP
;  CURRENT APPLICATION NUMBER: US/09/535,459
;  CURRENT FILING DATE:  2000-03-24
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2170
;  SOFTWARE: PERL Program
; SEQ ID NO 1891
;   LENGTH: 259
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00161335
;   NAME/KEY: unsure
;   LOCATION: 104, 238
;   OTHER INFORMATION: a, t, c, g, or other
US-09-535-459-1891

  Query Match              3.7%;  Score 57;  DB 10;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-18;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          18 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGT 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          59 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGT 3


RESULT 9
US-09-535-459-1881
; Sequence 1881, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
;  FILE REFERENCE: PD-1014 CIP
```

; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1881
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00212947
; NAME/KEY: unsure
; LOCATION: 23, 81, 171
; OTHER INFORMATION: a, t, c, g, or other
US-09-535-459-1881

Query Match 3.7%; Score 57; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTG 75
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 24 GCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTG 80

RESULT 10
US-09-535-459-1892/c
; Sequence 1892, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1892
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00190334
; NAME/KEY: unsure
; LOCATION: 158, 160, 237, 267
; OTHER INFORMATION: a, t, c, g, or other
US-09-535-459-1892

Query Match 3.7%; Score 57; DB 10; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGT 74
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 107 AGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGT 51

RESULT 11
US-09-535-459-1882
; Sequence 1882, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULES
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1882
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00209119
; NAME/KEY: unsure
; LOCATION: 23, 25, 126
; OTHER INFORMATION: a, t, c, g, or other
US-09-535-459-1882

Query Match 3.6%; Score 56; DB 10; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.2e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTGA 76
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 26 CTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGTGA 81

RESULT 12
US-09-535-459-1884/c
; Sequence 1884, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULES
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1884
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00083975
; NAME/KEY: unsure
; LOCATION: 2
; OTHER INFORMATION: a, t, c, g, or other
US-09-535-459-1884

Query Match 3.2%; Score 50; DB 10; Length 262;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 AGTCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTC 168
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 110 AGTCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTCCGCCATCTTC 61

RESULT 13
US-09-535-459-1889/c
; Sequence 1889, Application US/09535459

```
; Publication No. US20030040615A1
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
;  FILE REFERENCE: PD-1014 CIP
;  CURRENT APPLICATION NUMBER: US/09/535,459
;  CURRENT FILING DATE:  2000-03-24
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2170
;  SOFTWARE: PERL Program
; SEQ ID NO 1889
;   LENGTH: 280
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00204309
;   NAME/KEY: unsure
;   LOCATION: 2, 20, 230, 260, 268, 273
;   OTHER INFORMATION: a, t, c, g, or other
US-09-535-459-1889

  Query Match             2.8%;  Score 44;  DB 10;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 GCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGT 74
              ||||||||||||||||||||||||||||||||||||||||||||
Db        144 GCAATCTCACAGAAGGGGTTCATGGAGTGCTTCACACCATCAGT 101


RESULT 14
US-09-995-225-7
; Sequence 7, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Ruoping
;  APPLICANT:  Chu, Zhi Liang
;  APPLICANT:  Dang, Huong T.
;  APPLICANT:  Lowitz, Kevin P.
;  APPLICANT:  Pride, Cameron
;  TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0308
;  CURRENT APPLICATION NUMBER: US/09/995,225
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: 60/253,404
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/255,366
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/270,286
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/282,365
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/270,266
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/282,032
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,358
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,356
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/290,917
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: 60/309,208
;  PRIOR FILING DATE: 2001-07-31
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-7

  Query Match             2.8%;  Score 44;  DB 9;  Length 1086;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 701


RESULT 15
US-09-992-331-1
; Sequence 1, Application US/09992331
; Publication No. US20030022186A1
; GENERAL INFORMATION:
;  APPLICANT: FEDER, JOHN N.
;  APPLICANT:  MINTIER, GABE
;  APPLICANT:  RAMANATHAN, CHANDRA S.
;  APPLICANT:  HAWKEN, DONALD R.
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY18,
;  TITLE OF INVENTION:  EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: D0048NP
;  CURRENT APPLICATION NUMBER: US/09/992,331
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/308,540
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/261,782
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: 60/248,483
;  PRIOR FILING DATE: 2000-11-14
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-992-331-1

  Query Match             2.8%;  Score 44;  DB 10;  Length 1086;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 895
              ||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGACTGGTCATTGTGATCAGTTACTCCAAAATTTTACAGATCAC 701


Search completed: October  1, 2004, 04:22:21
Job time : 733.589 secs
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